

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 129485

TO: Mary Mosher

Location: REM/3D25/3C18

Art Unit: 1648

Monday, August 23, 2004

Case Serial Number: 09/851410

From: Toby Port

Location: Biotech-Chem Library

REM-1A59

Phone: (571) 272-2523 toby.port@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

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Mosher, Mary

Sent:

Tuesday, August 10, 2004 8:17 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence search 09/851410

Please translate & search AA encoded by:
nt 5147-7129 of SEQ 6
nt 5117-7096 of SEQ 10
And search SEQ 8.
Please do regular search, oligo search for the seq 6 & 10 translation products, and interference search. Thanks.

Mary Mosher AU 1648 571-272-0906 Office Rem 3D25 Mail Rem 3C18

STAFF USE ONLY

Searcher: ______Searcher Phone: 2-Date Searcher Picked up: _____Date Completed: _____Searcher Prep/Rev. Time: _____Online Time: _____

Type of Search
NA Sequence: #_
AA Sequence : #_
Structure: #_
Bibliographic:
Litigation:
Patent Family:
Other:

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other(Specify):

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August 21, 2004, 08:42:47; Search time 7642.28 Seconds (without alignments) 11246.543 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR002160 Sequence 1 AR021465 Sequence AR021465 Sequence AR021465 Sequence AR021615 Sequence AR021615 Sequence AR07631 Sequence AR07631 Sequence AR07631 Sequence AR07631 Sequence AR07631 Hepatitis E D10330 Hepatitis E D10330 Hepatitis E D10330 Hepatitis E C17109 Hepatitis E AR051830 Hepatitis E AR051830 Hepatitis E AR211247 Sequence AR07633 Hepatitis E AR07634 Hepatitis E AR07634 Hepatitis E AR07634 Hepatitis E AR076403 Hepatitis E AR076403 Hepatitis AR05668 Hepatitis AR05664 Hepatitis AR05664 Hepatitis AR05664 Hepatitis AR076354 Hepatitis	linear PAT 03-APR-1998
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AR002160	/organism="unknown" /mol_type="unassigned DNA" IGIN Query Match Best Local Similarity 100.0%; Score 1983; DB 6; Length 2049; Best Local Similarity 100.0%; Pred. No. 0; Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps ATGCGCCTCGGCCTATTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGCGCCAA	າ ບ—ບ ∢—∢	181 CCCTTCGCCCCCGATGTCACCGCTGCGGGGCTGGACCTCGTGTTCGCCAACCCGGC 24		Qy 421 TCTCCCCTTACCTCTTCGGGGCACTAACCTGGTTCTTTATGCCGGCCCCTCTT 480 Db 421 TCTCCCCTTACCTCTTCCGTGGCCACCAGACTTCTTATGCCGCCCCTCTT 480 Qy 481 AGTCCGCTTTTACCCCTTCAGGCGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540 Db 481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATAATGGCCACGGAAGCTTCT 540	AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC

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	RESULT 3 AR170404 AR170404 AR170404 BEFINITION Sequence 1 from patent US 6291641. ACCESSION AR170404 A	y Match Local Similarity 100.0%; Score 1983; DB 6; Length 2049; Local Similarity 100.0%; Pred. No. 0; hes 1983; Conservative 0; Mismatches 0; Indels 0; Gaps 1 ATGGGCCTGGGCTATTTTGTTGCTGCTCTATTTTTGCTATGCTGCCGGCCA 60	CGGCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGC	241 CGACCACTCGGCTTGGCGTGACCAGGGCCCCGCCGCCGTCGCTGCGT 300 301 AGACCTACCACCCGCTTGGCGTGACCAGGCCCCGCCCGTGCCTCACGTCGT 300 301 AGACCTACCACCAGGGCCGCGCTAACCGCGTCGCTCCGGCCCATGACACCCCG 360 301 AGACCTACCAGGCCGCGCGCGCTAACCGCGTCGCTCCGGCCCATGACACCCCG 360 361 CCACTACCAGGCCTGGGCCGCTAACCGCGTCGCTCGGCCCGTATAACCTACACCA 420 361 CCACTGCCTGATGTCGACTCCCGCGGCCCATCTTGCGCCGCAGTATAACCTATCAACA 420 421 TCTCCCCTTACCTCTTCCGTCGCCCCCCTACCTAACCTGGTTCTTTATGCCGCCCCTTT 480 421 TCTCCCCTTAACTCTTCCGTCGCCACCACCACACACTAACCTGGTTCTTTATGCCGCCCCTCTT 480 481 AGTCCGCTTTAACCCTTCAGGACGGCACCAATACCCTATAATGCCGCCCCTCTT 480

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Krawczynski,K.Z. and Yarbough,P.O.
Hepatitis B virus vaccine and method
Patent: US 6455492-A 1 24-SEP-2002;
Location/Qualifiers
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PPPAPDPSPPPBAALABPAGGATAGAPAITHGTARHRILLFYYPOGSKVFAGSLFES
TCTWLVNASNVDHROGGGLGHAFYORYPASFDAASFWNRDGAAAYTLTPRPITHAVAP
PRILAHNFRIDAAYRELTATTEDVATANIATISLISATDVGRACAGGRYTPGYVOYOF
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                                                                       /organism='Hepatitis E virus'
                                                                                                 /product='structural protein'
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Double;
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Takeda,N., Ri,T. and Miyamura,T.

HEPATITIS E VIRUS HOLLOW PRRITCLE, GENE ENCODING THE SAME AND PREPARATION OF RECOMBINATION VECTOR CONTAINING THE GENE AND UTILIZATION OF THE RECOMBINATION VECTOR.

L PATENT: JP 1998234383-A 3 08-SEP-1998;

DENKA SEIKEN CO LTD, KOKURITSU KANSENSHIYOU KENKYUSHO
OS HEDATILIS E VIRUS
PD 08-SEP-1998
PP 28-FEB-1997
PP 1997062445
PI TAKEDA NAOKAZU, RI TENSEI, MIYAMURA TATSUO
PC CI2N15/09,C07K14/08,C12N5/10,C12P21/02;
                                                                                      GACCAGTCCACTTATGGCTCTTCGACTGCCCAGTTTATGTTTCTGACTCTGTGACCTTG
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QY 1921 CAGTCTACTGTGAGCTTCAGGGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980 Db 1921 CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTA 1980 QY 1981 TAG 1983 Db 1981 TAG 1983	RESULT 11 E17109 LOCUS DEFINITION Hepatitis E virus gene. ACCESSION E17109 VERSION E17109.1 GI:5711792 KEYWRDS JP 1998234383-A/5.	NIS ORS	JOURNAL PARENT: UP 1998.2449. A 06.5EF.199; COMMENT OS Hepatitis E virus COMMENT ON 1999.24483-A/5 PD 08-SEP-1998 PF 28-FEB-1997 UP 1997062445 PI TAKEDA NACKAZU, RI TENSEI, MIYAMURA TATSUO PC C12M15/09, COTK14/08, C12M5/10, C12M21/02;	CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers FH	inos	/mol_type="genomic DNA" /db_xref="taxon:32644" ORIGIN	Query Match 98.3%; Score 1949.4; DB 6; Length 7194; Best Local Similarity 98.9%; Pred. No. 0; Matches 1962; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	2y 1 Algegeerreggeerregreergerregreerregreerreggeer 60	QY 61 CCGCCCGGTCAGCCGTCTGGGCGCCGTCGTGGGCGCGCGGTTCCGGCGGTGGT	OY 121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	QY 181 CCCTTCGCCCCGATGTCACCGCTGCGGGGCTGGACCTCGTGTTCGCCAACCCGCC 240	Oy 241 CGACCACTCGGCTTGGCGTGACCAGGCCCCGCCGTTGCCTCACGTGCT 300 Db 5387 CGACCACTCGGCTTGGCGTGACCAGGCCCCGCCGCCGTTGCCTCACGTCGT 5466	Oy 301 AGACCTACCACAGCTGGGGCCGCTAACCGCGGTCGCTCGGCCCATGACCCCG 360
781 GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840 841 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACGGGTGCCCTCGGGCTGTTG 900	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCGGGGGGGGGG	1081 GTGGTGAGATCGGCCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT	1201 GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAATGCTCAG	CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC	1381 CCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT	1441 GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 1500	1501 GITAATGITGCGACCGCGCGCGCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACA 1560 	1561 CTIGAGGICGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG 1620 1561 CTIGAGGGTCGCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG 1620	1621 CTCCGCGGTAAGCTCTTTCTGGGAGGCAGCCAAACTAAAGCCGGGTACCCTTATAAT 1680 	1681 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCT 1740 	1741 ATTICCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 1800 	1801 TTAGCCCCCACTCTGCGCTAGCATTGCTTGAAGATACCTTGGACTACCCTGCCCGGCC 1860 	1861 CATACTITIGAIGATITCIGCCCAAGAGGCCGCCCCTIGGCCTTCAGGCTGCGCTTTC 1920

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AVARSLDWTKVTLDGRPLSTIQQYPKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTTAS
DQLLVENAAGHRVALSTYTGSLGAGPVSISAVAVLAAHSALALLEDTLDYPACAHTFD
DFCPECRPLGLQGCAFQSTVABLQRLKMKVGKTREL"
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PDESAPCRETAIRKALSKFCCFWKRIGGECTFLOPAEGYVGDOGHDRRYLGSBYD
PAESAISDIS GSSYVUPGTALOELYGALDLEPEI VARAGRITATYKVGQVDGRIDCETL
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FCCSRLMYTKLRGISKYVVGTLVANBGWNASEDALTAVITAAYLTICHQRYLRTQAIS
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RICHGSPWNSYTNTPYTGALGLEDFRALELERNATTRVRYRSYSSTARHRARRG
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EKNWGPGPERAEQLRLAVSDFLRKLTNVAQMCVDVVSRVYGVSPGLVHNLIGMLQAVA
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TTAGAAPLTAVAPAHDTPPVPDVDSRAAILRRQYNLSTSPLTSSVATGTNLVLYAAPL
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                                 Fax:81-3-3972-8830)
Submitted (23-Jan-1992) to DDBJ by:
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Nihon University School of
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                                                                                   Toshikazu Uchida
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Itabashi-ku, T
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DFCPECRPLGLQGCAFQSTVARKVGKTREL
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gene, complete cds.
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SPLLPLQDGTNTHIMATEASNYAQXRVARATIRYRPLVPNAVGGYAISISFWPQTTTT
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Direct Submission
Submitted (28-JAN-1999) Hepatitis, National Institute of 20-A Dr. Ambedkar Road, Pune, Maharashtra 411001, India Location/Qualifiers
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Arankalle, V.A., Paranjape, S., Emerson, S.U.,
Wallmbe, A.M.
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E-like viruses.
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/mol_type="genomic RNA"

/isolate="AKL-90"

/db_xref="taxon:12461"

/country="India"
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/product="ORF-2"
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TAGVPGSGKSRS ITQADVDVVVVPTRELRNAWRRGFAAFTPHTAARVTGGRRVVIDB
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CPELEQGLLYLPQELTTCDSVVTFELTDIVHCRMAAPSQRKAVLSTLVGRYGRRTKLY
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BYDDTVFSAVAARASMYNFENDFSEDSTQMYSLGLEGAMGGGRAPQMISLXLYH
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SIVLCSEYRQSPGAAVLIAGGGGLKLKVDFRPIGLYAGVVVAPGLGALPDVVRFAGRLT
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MLCIHGSPVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRG
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DFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL"
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VHRCFLRPVGRDVQRWYTAPTRGPAANCRRSALRGLPAADRTYCFDGFSGCSFPPETG
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                                                                                                                                  of experimentally infected
                                                                                                                                                                                                      /product="immunogenic protein"
/protein_id="AAC97187.1"
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            E virus"
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                                                                                                                                /note="isolated from the
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/db xref-":
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28. .5109
                                                                                                         /country="Nepal"
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/note="ORF2"
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                                           Gaps
     DB 14; Length 7199;
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                                         54; Indels
   Score 1896.6;
Pred. No. 0;
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95.6%;
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                                                                                                                 CTTGATGGCCGCCCTCTCTCCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG
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                 CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
                                                                            GTTGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                                                                                                       GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
                                                                                                                                                                                                           CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGTTATT
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                                                                                                     <u> GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC</u>
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AF185822 7143 bp RNA linear VRL 14-JUN-2001 Hepatitis E virus nonstructural polyprotein gene, partial cds;

RESULT 15 AF185822 LOCUS DEFINITION

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VGRDVQRWYTAPTRGPAANCRRSALRGLPAADRTYCFDGFSGCSFPAETGIALYSLHD
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YLRGISKVYTVGTLVYBNEGWNASEDALTAVITAAYLTICHQRYLLTRDS
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APGVSEYLYTYTRWBEVDAVSSPARPDLGFWSEPSISSRAATPTLAAATPLAFAPDLS
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SNADHRPGGGLCHAFYQRYPASFDAASFVWRDGAAAYTLTPRPITHAVAPDYRLEHNP
KERBAYRFTGSRLCTGTAAYPLLGTGTYTQVPICGTSFDAWBRNHSFDBETYLLFBLENP
EANRPTRPALITTEDVARTAALAI ELDSATTVGRACAGCRVTPGVVOYOFTAGVPGGG
KSRSITQADVDVVVVPTRELRNAMRRRGFAAFTPHTAARVTGGRRVVIDEAFSILPPHL
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ISGSYVVPGAALQPLYQALDLPAEIVARAGRLTATVKVSQVDGRIDCETLLGNKTFRT
SFVDGAVLETNGPERHNLSFDASQSTWAAGPFSLTYAASAAGLEVRYVAAGLDHRAVF
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ISACYPHIQTYTERULRELPERBAVGOLUVFTQARAAROESVTVHEAGCATVTETTII
ATADARGLI COSSRAHAIVALFHENCVI IDAPGLIABEVGI SDAI VNNFFLAGGEI GH
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LYLPOBLITTODSVVTFELTDI VHRRMAAPSQRRAVLSTLVGRYGRRATLYNASHBDVR
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KFTTGFFI TAHGKVGGGI SAMSKTFCALFGPWFRAI EKAILALLDLONRDSRI IFFORDCIN
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OPKESLEKPWKKHSGEPGTLIMNTYMMAVITHCYDFRDLQYAAFKODSIVLCGEY
ROSPGAAVILIAGCGIKLKVDFRPIGILYAGVVVAPQLGALPDVVRFAGFLTEKWWGPGP
ERAEQLRLAVSDFLRKLINVAQMCVDVVSRVYGVSPGLVHNLIGMLQAVADGKAHFTE
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Caudill,J.D., Snellings,N.J., Begot,L., Innis,B.L., Longer,C.F. and
                                                                                                                                                                                                                                                                                                       1 (bases 1 to 7143)
van Cuyck-Gandre, H., Zhang, H.Y., Tsarev, S.A., Warren, R.L.,
Caudill, J.D., Snellings, N.J., Begot, L., Innis, B.L. and Longer, C.F.
Short report: phylogenetically distinct hepatitis E viruses in
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                                                                                                                               Hepatitis E virus
Hepatitis E virus
Viruses; BSRNA positive-strand viruses, no DNA stage; Hepatitis
E-like viruses.
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Ticchurst, J.
Ticchurst, J.
Direct Submission
Submitted (13-SEP-1999) Agents Transmissibles, CRSSA, 24 Ave Maguist du Grasivausan, BP 87, La Tronche 38702, France
Location/Qualifiers
1. 7143
protein gene, complete cds; and unknown gene.
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/note="ORF3"
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1801 TTAGCCCCCCACTCGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCGGGCC 1860	6896 TIAGCCCCCCACTCTGCGCTAGCTTGATTGTTTGTTTGGATACCTTGGATTACCCTGCCCGCGCC 6955	1861 CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGCTGCGCTTTC 1920	6956 CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTCCAGGGCTGTGCTTC 7015	1921 CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980	7016 CAGICTACTGTCGCTGAGCTTCAGCGTCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTA 7075	1981 TAG 1983	7076 TAG 7078	
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Search completed: August 21, 2004, 15:14:59 Job time : 7653.28 secs

Jan Shao

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E virus; Burma; Mexico; immunoassay; peptide antigen; antibody; HEV; ds.
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AAQ27436
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AAV66322
AAV54730
AAA99260
AAF83496
AAL50387
ADD24378
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ADE06696
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89US-0036672.
89US-00420921.
90US-00505888.
91US-00621078.
92US-0082335.
92US-00876941.
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P-PSDB; AAW35826
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17-JAN-1992;
20-APR-1992;
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11-APR-1989;
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13-OCT-1989;
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Compugen Ltd.
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                                                                                                                                          3373863 seqs, 2124099041 residues
                                                                                     US-09-851-410A-6_COPY_5147_7129
       GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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                                                             A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence encodes the protein from the open reading frame, ORP2, from HEV burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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P-PSDB; AAR96089.
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13-OCT-1995;
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Immunogenic hepatitis B virus (HEV) peptides are selected from the ORF1, ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to prevent infection by HEV. The antibodies can neutralise and block HEV infection and can be used to prevent or treat HEV infection. The peptides and antibodies can also be used as diagnostic reagents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1, ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.
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The present sequence represents the genome of the Burma strain of enterically transmitted non A non B hepatitis virus (ET-NANB) (hepatitis be rirus (HEV)). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF) sequence from Burma HEV isolate. The protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-2003 to correct OR field.)
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          diagnosis or vaccine production
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          - useful for
                                                                   51-58; 47pp; English
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        Hepatitis E virus proteins
the virus.
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Best Local Similarity 100.
Matches 1983; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmitted non A non B hepatitis virus; ET-NANB; virus; HEV; Burma HEV isolate; vaccine; diagnostic probe; ds.
                                                                                                                                                                                                                                                    CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGCTTGCGCTTTC
ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGGTTGCCGTT
                                                                                                                                                                                                                            CATACTTTTGATGATTTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC
                                                                                                                                            TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC
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/note= " encodes AAW80197"
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/note= " encodes AAW80196"
5106. .5477
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/note= " encodes AAW80198"
5147. 7129
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P-PSDB; AAW80196, AAW80197, AAW80198
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89US-00367486.
89US-00420921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV66321 standard; DNA; 7195
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                            TAG 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                TAG 2028
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1990;
25-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterically
Hepatitis E
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23-DEC-1998
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non-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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720

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Enterically transmitted nonA/nonB hepatitis virus; identification; HEV; ET-NANB; detection; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the sequence of the Burmese isolate of enterically transmitted nonA/nonB viral hepatitis agent (ET-NAMB). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV), detecting ET-NAMB in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in vaccines. (Updated on 25-MAR-2003 to correct PF field.)
CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yarbough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E virus DNA - useful for e.g. virus detection and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7195 BP; 1221 A; 2312 C; 1868 G; 1794 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                     sequence of the Burmese isolate of ET-NANB.
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                                                                                                                                                                                                                                                                                                                          /note= "see AAW71209"
5106. .5477
/*tag= c
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5147. .7129
/*tag= b
/note= "see AAW71210"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-446186/38.
P-PSDB; AAW71209, AAW71210, AAW71211.
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                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
28. .5109
                                                                                                                                                             BP.
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00505888.
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                                                                                                                                                             AAV54729 standard; DNA; 7195
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                                                                                                                                                                                                       (revised)
(first entry)
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                                                                                  TAG 1983
                                                                                                     TAG 7129
                                                                                                                                                                                                                                                                                               Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1988;
11-APR-1989;
19-JUN-1989;
13-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              US5789559-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-AUG-1998
                                                                                                                                                                                                        25-MAR-2003
30-OCT-1998
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05-APR-1991
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                                                                                  1981
                                                                                                       7127
                                                                                                                                                                                   AAV54729;
                                     1921
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                                                                                                                                     AAVS4729
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                                                                                 Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein; immunological; diagnosis; hepatitis; infection; identification; detection; immunoreactive; hepatotropic; antiinflammatory; virucide; vaccine; antiviral; antigenic; antibody; antigen; ds.
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Krawczynski KZ,

Bradley DW,

Yarbough PO,

TECHNOLOGIES INC

DEPT HEALTH & HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated DNA comprising the genome of an enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also referred as HEV). The DNA sequences or their fragments are useful in preparing ET-NANB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The present sequence represents a ET-NANB viral DNA sequence from HEV-Burma strain
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                                                                                                                                                                   New DNA sequences of enterically transmitted non-A/non-B (ET-NANB) hepatitis viral agent, useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
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P-PSDB; AAB62522, AAB62523, AAB62524.
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HEV; enterically transmitted nonA/nonB viral hepatitis agent; viral; ET-NANB; infection; vaccine; ds.

Hepatitis E virus.

ET-NANB viral DNA sequence from HEV-Burma strain.

(first entry)

23-JUL-2001

AAF83495

BP

AAF83495 standard; DNA; 7195

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                                                                                                                                                                                                                                                               GCTGTCGGCGGTTACGCCATCTCCATCTCTGGCCACAGACCACCACCACCCGGACG
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                                                                                                                                                                                                           The invention relates to a protein derived from an enterically transmitted non-A/non-B viral hepatitis agent. The viral proteins are useful for detecting infection by the enterically transmitted non-A/non-B viral agent. The proteins are also useful for producing vaccines for immunising an individual against HEV hepatitis viral agent. The DNA fragments are useful for identifying and sequencing the entire viral agent and for assaying the viral agent in an infected sample. The present sequence is used in the exemplification of the
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                                                                                                     roteins derived from an enterically transmitted non-A/non-B (ET-viral hepatitis agent, useful for diagnosing ET-NANB infection and cing vaccines for immunizing an individual against ET-NANB hepatitis
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              Bradley
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Best Local Similarity 99.8%;
Matches 1980; Conservative
              Yarbough PO,
                                                           WPI; 2003-810978/76.
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89US-00336672.
89US-00420921.
90US-00505888
91US-00681078.
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
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05-APR-1991;
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03-AUG-1998
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     ATTTCCACTTACACCACTAGCCTGGGTGCTGCTCCATTTCTGCGGGTTGCCGTT
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                                                                                                                                                                                                                                                                                                                                   enterically transmitted non-A, non-B hepatitis virus; hepatitis C; E.coli strain BB4; ATCC deposit number 67717; Burma; ss.
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5106. .5477
//taga = "ORF 3"
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P-PSDB; AAR14618, AAR14619, AAR14620.
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cynomolgus monkeys infected with the Burma strain of ET-NANB. Both strands of ET1.1 were sequenced. Identity of the sequence with sequences in ethologic agents has been confirmed by locating a similar sequence in a viral strain isolated in Burma. The sequence of the Burma strain is given here. See AAQ141.0 for ET1.1. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible
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Pred. No. 0;
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(KOKU-) KOKURITSU YOBO EISEI
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encoding it - useful for more accurate detection of HEV immuno-assays and nucleic acid hybridisation.
                                                                                                                                                        7194 BP; 1217 A; 2312 C; 1871 G; 1794 T;
                                                                                                                                                                                 DB 2;
                                                                                                                                                                               Score 1949.4;
Pred. No. 0;
0; Mismatches
                                        Disclosure; Page 27-29; 29pp; Japanese
                                                                                                                                                                                 Query Match 98.3%;
Best Local Similarity 98.9%;
Matches 1962; Conservative
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                                                                                                                                                                                                                                                                            HEV; ORF2; antigen; vaccine; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Torresi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MACF-) MACFARLANE BURNET CENT MEDICAL
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          CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
                                                               GACTTTGCCCTTGAGCTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC
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1261 CAGGATRAGGGTATTGCDATCCCGCATGACCTCGGAGAATCTCCTGTGGTTATT 1220	RESULT 15 ABL60053 LD ABL60053; XX AC ABL60053; XX AC ABL60053; XX DT 16-AUG-2002 (first entry) XX XX BE Hepatitis E virus ORF-2 DNA #1. XX COS Hepatitis E virus. XX
TECTOGGGGGGGTGACCGGGGTGACTCCCCTTCGCAATCCCCTATATCATCCAACCAA	### TCCGGTTATTCCAGCACTGCCACCGCGGGGGGGGGGGGG
121 TTCTGGGGTGACCGGGTTGAN 181 CCCTTCGCCCCGATGAN 181 CCCTTCGCCCCCGATGTCAC 241 CGACCACTCGGCTCGGCTG 241 CGACCACTCGGCTCGGTTG 301 AGACCTACCACTGGGTGGGGC 361 CCAGTGCCTACTGGTGGGCC 421 CCCGTTGACTTTGACTCGTTGACTC 421 TCTCCCCTTACTTTGACTCGTTGACTC 421 TCTCCCCTTACTTTGACTCGTTGACTC 421 TCTCCCCTTACTTTGACTCGTTGACTCGGTTGACTCGGGGGGGG	961 TCCGGTATTCCAGCACTGG 961 TCCGGTTACTCCAGCACTGG 1021 CTCACCACCAGGCTGCTAC 1021 CTTACCACCAGGCTGCTAC 1081 GTCGGTGAGATCGCCGCG 1081 GTCGGTGAGATCGCCGCG 1141 GGCGGCCTGCCGACAGAAT 1141 GGCGGCCTGCCGACAGAAT 1141 GGCGGCCTGCCACAGAAT 1151 GGCGGTCTACCGACAGAAT 1161 GGCGGTCTACCGACAAAT 1161 GGCGGTCTACCGACAAAT 1161 GGCGGTCTACCGACAAAT 1161 GGCGGTCTACCGACAAAT 1161 GGCGGTCTACCGACAAAT 1171 GGCGGTCTACCGACAAAT 1171 GGCGGTCTACCGACAAAT 1171 GGCGGTCTACCGACAAAT 1171 GGCGGTCTACCGACAAAT 1171 GGCGGTCTACCGACCAATGGCGG

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invention relates to novel n-mer polypeptides comprising amino acids of ORF-2 of HEV where n = 2-180. The polypeptides of the invention have virucide activity. The polypeptide of HEV, its fragments, and chimeric proteins, are useful for vaccine compositions and diagnosis in preventing and treating HEV infection by immunisation, which may also be applied in the diagnosis of HEV infection (HEV) for vaccine compositions Polypeptide fragments of hepatitis B virus (HEV) for va and diagnosis in preventing and treating HEV infection. 2; He × Example 1; Page 82-83; 91pp; Chinese g ŝ g ဥ TANG Z WPI; 2002-427096/45. SHENG ٦,

Length 1990; T; 0 U; 0 Other; . 9 B Sequence 1990 BP; 348 A; 666 C; 481 G; 495 Query Match

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1020 1020 1080 1080 1140 1140 1200 1200 1260 1260 1320 1320 1380 1380 1440 1440 1500 1500 1560 1620 1620 1680 1800 1680 1740 1740 780 840 840 900 900 096 720 960 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG GCCTCCGAGCTTGTTATCCCAAGTGAGCGCCTACACTACCGTAACCAAGGTTGCCGTTGTT GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC GACTITIGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCCAATACGCGGGTC TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGGACGGGACTGCCGAG TCCCGTTACTCCAGCACTGCCCGTCACCGCCTTCGTCGCGGTGCAGAGGGACTGCCGAG GTCGGTGAGATCGGCCGTGGGATAGCGCTTACCCTGTTTAAACCTTGCTGACACCCTGCTT GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGTATT GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCTGTTCAACCTTGCTGACACTCTGCTT GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCGTCCC CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC CCTTICTCTGTCCTTCGAGCTAATGATGACTTTGGCTCTCTCTCACCGCTGCCGAGTAT CTCACCACCACGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT ctraccaccaccaccccracccccrrcarcaaccaccrcrartracracracraarcc CAGGATAAGGGTATTGCAATCCCGCATGACATCGACCTCGGGGAGTCTCGTGTATTT certititiciciceceaectaateatetecriticecriticicicicaeceaetar GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTTCTGTGACCTTG GACCAGTCCACTTACGGCTCTTCGACCGGCCCAGTCTATGTCTCTGACCTCTGACCTTTG CTCCGCGGTAAGCTCTCCTTTTGGGAGGCAGGTACTACTAATAATCTCCGTATACCTTATAAT TATAACACCACTAGTGACCAACTGCTCGTTGAGAATGCCGCTGGGCATCGGGTTGCT ATTTCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT GTTAATGTTGCGACCGCGCGCGCGGTGCCCGGTCGCTCGATTGGACCAAGGTCACA CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG CTCCGCGGTAAGCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT 841 721 721 781 901 781 841 1021 1021 1081 1081 1141 1141 1201 1261 1261 1381 199 901 196 961 1201 1321 1321 1381 1441 1441 1501 1501 1561 1561 1621 1621 1681 1681 1741 ⋧ 셤 ò Q g g ð ò ò g δ g õ g à g ò ద δ 셤 8 8 Q DP à qq 8 8 8 g à g ò g ò

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OY 1801 TTAGCCCCCACTTGCGTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGGCC 1860

Db 1801 TTAGCCCCCCACTCGGGTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGGCC 1860

OY 1861 CATACTTTTGATGATTTCTGCCCGAGGTGCCCCCTTGGCCTTCAGGGCTGCCCGGCC 1800

Db 1921 CAGTCTTTCGATGATTTTGCCCGGAGTGCCCCTTGGCCTTCAGGGCTGCTTTT 1920

OY 1921 CAGTCTACTGTCGCTGAGGCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTTT 1920

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BX360624 BX360624 CG747711 P041-2-E0 BX34968B BX34968B AL056652 Drosophil BX446579 BX446579 AL054280 Drosophil CG754612 P050-1-D0 AL099352 Drosophil CD608311 CR20-1-D0	BM560246 AGBNCOURT CC290874 CH261-172 BE574895 msh2 4207 CG748837 po42-4-E0 BX464554 BX464554 AL066051 Drosophil CD507542 CD86-G02 AG135089 Pan trog1l BX407619 BX407619 BX391246 BX391246 BX56926 pacs2-164 CC219663 CH261-165 AL065254 Drosophil BX608152 AGBNCOURT	CD50997 BX421125 AG0125 AG0125 CC189908 CX78818 BQ68081 BQ68081 BM556092 BM556173 BC051751 BC061197 AG1867751 BX415111 BW838409 AL550172	bp DNA linear GSS 03-JUN-1999 le survey sequence TET3 end of BAC # from Drosophila melanogaster (fruit t fly) a; Hexapoda; Insecta; Pterygota; era; Brachycera; Muscomorpha; rosophila. cope - Centre National de Sequencage: NCE (E-mail: seqref@genoscope.cns.fr sequence was carried out as part of a y Drosophila Genome Project (BDGP). ysical map of the Drosophila se BACs. For further information ly. org The BDGP Drosophila ly. org The BDGP Drosophila prepared by Kazutoyo Osoegawa and ong's laboratory in the Department of
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen.FRATURES Location/Qualifiers Contact : Feng Liang Email
: fliang@lifetech.com URL : http://fulllength.invitrogen.com/
InvitroGen.Corporation 1600 Faraday Avenue Genoscope sequence ID:
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digested with Not I and cloned into the Not I and CORY v
sites of the pCMVSPORT 6 vector. Library was normalized."
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(Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full.length cDNA libraries and normalization
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Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODK005AAlOQP1.
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clone CSODIO15YN12 3-PRIME, mRNA sequence.
BX335523.1 GI:30312422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Mismatches 164;
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Similarity 39.7%; Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BOGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP from the land BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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1. (bases 1 to 1201)

1.i., W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12943429.

Contact: Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
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AL578906
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 584.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODKO05AA10QPl&cluster=584.f. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 CCGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTC
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/clone lib="RPCI-98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .larity 12.4%; Pred. No. 0.0001;
Conservative 180; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.4%; Score 67.2; 12.4%; Pred. No. 0.
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Matches 44; Conserv
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                     96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        548
                                                                                 /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                            907 YRTCTCTCTYGACCKSSSSBGGSGSGTCKCGGGTTTCGTTYATCCGSCCCCCCACCCC 848
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Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com thttp://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1103)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDMA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                4.
                                                                                                                                                                                                                          ; Score 63.6; DB 13; Length 1201;
; Pred. No. 0.00083;
51; Mismatches 203; Indels 4;
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Genoscope - Centre National de Sequencage
                  organism="Homo sapiens"
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                                                 xref="taxon:9606"
                                                                 /clone="CS0DI015YN12"
                                  'mol_type="mRNA"
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/tissue type="PLACENTA"

/clone lib="Homo sapiens PLACENTA"

/cone lib="Homo sapiens PLACENTA"

/note="Wector: PCMVSPORT 6; 1st strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECRNV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CS0DI072YL05 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 GGCGCAGCGGCGGTTCCGGCGGTGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCG 154
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.r
Contact : Feng Liang Bmail: | Iliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO72CF03NPI.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1103;
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FP1
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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29.2%; Pred. No. 0.0017;
iive 89; Mismatches 144;
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Genoscope - Centre National de Sequencage
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                                                                                 /organism="Homo sapiens"
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                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BA007ZH12"
                         Location/Qualifiers
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BX360624.1 GI:30376452
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BX349688 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CS0DI063YK05 3-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7092.r For
more information about this cluster, see
http://www.genoscope.nns.fr/
cgi-bin/cluster.cgi?seq=CSOBAHO15ZB03NP1&cluster=7092.r. Contact
Feng Liang Email: fliang@lifetech.com VRL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAHO15ZB03NP1.
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Best Local Similarity 37.2%;
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Srinivasan, J., Sinz, Jesse, T., Wiggers-Perebolte, L., Jansen, K.,
Buntjer, J., Shar Meulen, M. and Sommer, R.J.
An incegrated physical and genetic map of the nematode Pristionchus
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/db xref="taxon:9606"
/clone="CSODIO72YL05"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ist strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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9.2%; Pred. No. 0.0052;
ative 163; Mismatches 8
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                               CITCGCAATCCCCTATATTCATCCAACCAACCCTTCGCCCCCGATGTCACCGCTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                               210 CGGGGCTGGACCTCGTGTTCGCCAACCCGGCCGACCACTCGGCTCCGCTTGGCGTGACCA
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Ephydroidea, Drosophilidae, Drosophila
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0
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organism="Homo sapiens"
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                   /mol_type="mRNA"
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                                                          /clone="CS0DI063YK05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
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Drosophila melanogaster
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KEYWORDS
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ORGANISM
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CNS0052P/c
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EACRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          For
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cgi-bin/cluster.cgi?seq-CLOBB002ZFI0FPl&cluster=7325.f. Contact
Feng Liang Email: fliangalifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBB002ZF10FP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SBBGGGSSSKTSGSSSSCBSGSSSTGSSGSKXSSSTSSSSSGCGTGKNTTTGCVGS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 GIJGCIGCICCICAIGITITIGCCIAIGCIGCCCGCCCACCGCCCGGCCGGCCGICIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGCCGTCGTGGCGCGGCGGTTCCCGGCGGTGGTTTCTGGGGTGACCGGGTTGA
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BP 191 91006 EYRY cedex - France
Email: seqrefégenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7325.f
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BX446579 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB002ZF10 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 3.0%; Score 59.6; DB 29; Similarity 19.9%; Pred. No. 0.0061; 59; Conservative 127; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BACR11P16"
/clone_lib="RPCI-98"
/note="end : TET3"
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UG/54612 1793 bp DNA linear GSS 24-OCT-2003 P050-1-D08.za Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSGBSSGCSSSSGSSSSGSSSSGCSSSSGCGGCSTSCSSTTCSSBTSGKSSSGC 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ACCACTCGGCTTCGCCTTGGCGTGACCAGGCCCCAGCGCCCGCGTTGCCTCACGTCGTAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    578 STSSSSSTSGTSGSGTSSSCSTSCBTCCGCSCYSCCCCSCCSCTCCSCGT 519
Pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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                                                                                                                                                                                                                                                                                                                               Length 839;
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
                                                                                                                                        /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db xref="texon:7227"
/clone="BARRIOEG"
/clone lib="RRCI-98"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                               Score 59.2; DB 29;
Pred. No. 0.0076;
                                                                                                                                                                                                                                                                                                                                                                             129;
                                                                                                                                                                                                                                                                                                                                                                               65; Conservative 147; Mismatches
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Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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CG754612.1 GI:37980282
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                                                                                                                            1. .839
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BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr |
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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                                                                                                           /tissue type="NEUROBLASTOMA"
/ciose lib="Homos sapiens NEUROBLASTOMA"
/clone lib="Homos sapiens NEUROBLASTOMA"
/note="Wector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
couble-strand cDNA was digested with Not I and cloned into
the Not I and BORNY sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Beoptera; Endoptazoy, Arthropoda; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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llarity 36.0%; Pred. No. 0.0073;
Conservative 65; Mismatches 144;
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                       'organism="Homo sapiens"
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                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB002ZF10"
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                                                                                                                                                                                                                                                                                                                                                                143 CTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCCTTGGCCCCCGGATGTCACCG
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                                                                                                                           /note="The library was generated by a partial digest the genomic DNA with EcoRI and cloning into the BAC vector."
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AL099352
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/clone_lib="Ppa EcoRI BAC Library"
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organism="Pristionchus"
                             /mol_type="genomic DNA"
/strain="California"
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                library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbelobacil.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAACCAACCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGGCTGGACCTCGTGTTCGC 231
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGCGCCACCGCCCGGTCAGCCGTCTGGCCGTCGTGGCGGCGCGCAAGCGGCGGTTCC
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     -. This Drosophila melanogaster BAC
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
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/mol type="genomic DNA"
/clone="BACN04P24"
/clone lib="brosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 58.4; DB 29; 38.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (fruit fly)
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AL066742
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
http://www.edgp.ebi.ac.uk
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/clone="Chakon: 9223/
/clone="Chakon: 9223/
/tissue_type="heads and internal organs combined"
/tissue_type="heads and internal organs combined"
/dev stage="heads and internal organs combined"
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/clone_lib="wetcor: lambda ZAP Express/pBK-CMV; Site_1: EcoRl
/note="wetcor: lambda ZAP Express/pBK-CMV; Site_1: EcoRl
/s' adaptor); Site_2: MhoI (3' linker primer); The mixed
organ cDAP library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a 50 bp linker primer containing an oligo dT sequence
preceeded by a synthetic KhoI site. 5 prime adaptors were
used containing an EcoRl cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."
                                                                                                                          CA 94305-5329, USA
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      Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford,
Fal: 650 725 5954
Fax: 650 725 7739
Email: Kingsley@cmgm.stanford.edu
Plate: 90
                                                                                                                                                                                                                                                                                                                                                                                          organism="Gasterosteus aculeatus"
                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="Salinas river, CA"
                                                                                                                                                                                                                                                                                           High quality sequence stop: 172.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:69293"
Unpublished (2003)
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Best Local S:
Matches 163;
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Ringsley, D. M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGACACCCCGCCAGIGCCIGAIGICGACICCCGCGGCGCCAICTIGCGCCGGCAGIATAA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722
                              melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP from the plant of the Library and how to order individual BAC clones, the entire library. If litters for hybridization from the BACPRAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCGCCCACCGCCCGCCGTCAGCCGTCTGGCCGCTCGTCGTGGGCGCGCCCCAGCGGCGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 CCAACCCGCCCGACCACTCGGCTCCGCTTGGCGTGACCAGGCCCCAGCGCCCCGCCGTTGC
      genome using these BACs. For further information
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2.9%; Score 58; DB 29; Length 932;
Best Local Similarity 33.1%; Pred. No. 0.015;
Matches 120; Conservative 81; Mismatches 156; Indels
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7227"
/dlone="BACR14B09"
/clone lib="RRPCI-98"
/note="end : T7"
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/lab host="DH10B (phage-resistant)"
/clone_line="NIH_MGC_98"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site_2:
Cloned into BcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapDs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://mage.llh.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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612 TTACGCCATCTCCATCTCTGGCCACCACCACCACCACCCCGGACGTC
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larity 37.0%; Pred. No. 0.017;
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High quality sequence stop: 312.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-876-941A-1
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Listing first 45 summaries
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APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Yarbough, Patrice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
CORRESPONDENCE ADDRESS:
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ORF-2
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MEDIUM TYPE: Floppy disk
COMPUTER: Inha PC compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION IN-435
ATTORNEY/AGENT INFORMATION:
NAME: CARZIER K. Sholtz
RECIETRATION NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TVENEY NUMBER: ACIO
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US-09-462-606-3
US-09-462-606-3
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US-08-240-049B-2
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                      Genelabs Technologies, Inc
                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08240049B
Patent No. 5686239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genelabs TechnoloSTREET: 505 Penobscot Drive CITY: Redwood City STATE: CA COUNTRY: USA
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                                                                                                                                                                                      COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-UN-1994
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             APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE: INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      CLASSIPCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
FILING DATE: 13-OCT-1989
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PRIOR APPLICATION DATA:
APPLICATION .....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 324-0880 TELEPAX: (415) 324-0860 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : CDNA to mRNA
NO
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FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
Tam, Albert W.
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STRANDEDNESS: doub]
TOPOLOGY: linear
                                                                                                             STREET: 350 Camb
CITY: Palo Alto
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Best Local Simi
Matches 1983;
            APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
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100.0%; Pred. No. 0;
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REGISTRATION NUMBER: 38,615
TELEPOWINICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             CLASSIFICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-APPLI-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAM-1992
PRIOR APPLICATION NUMBER: US 50,888
FILING DATE: 17-JAM-1992
PRIOR APPLICATION NUMBER: US 50,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 11-APPRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APPRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APPRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-AUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: SHOLZ, CHAILES K.
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Best Local Similarity 100.
Matches 1983; Conservative
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MOLECULE TYPE: cD
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TOPOLOGY: lir
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           CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320
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                                   CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
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US-08-484-054-3
US-08-484-054-3
Sequence 3, Application US/08484054
Patent No. 5770689
GENERAL INFORMATION'
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tww, Ur-Shin
APPLICANT: Tww, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TILE OF INVENTION: Hepatitis E Virus Vaccine and
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
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301 AGACCTACGAGAGGGGGGGGGGGGGGTGGGTGGCTCCGGAGGACCCCG 360 	CAACA 	TCTCCCCTTACCTCTTCCGTGGCCACCGCCATACCTGGTTCTTATGCCGCCCTCTTTCTT	CHICH	CCAAT 	601 GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCGACG 660	GCATA 	721 GCCTCTGAGTCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780 	781 GTCGAGACCTCTGGGGTGGCTGAGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840 	rgrrg       rgrrg	3GGTC       3GGTC	961 TCCCGTTATTCCAGCACTGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020 	1021 CTCACCACGGCTGCTACCGGTTTATGAAGGACCTCTATTTACTAGTACTAATGGT 1080	1081 GTCGGTGAGATCGGCCGCGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT 1140 1081 GTCGGTGAGATCGGCCGCGGGGATAGCCCTCACCTTGCTGCACACTTGCTGCTT 1140	1141 GGCGGCCTCCCGACAGAATTGATTTCGTCGGCTGGCCAGCTGTTCTACTCCGTCC 1200	1201 GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG 1260 	1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320 	1321 CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATGGGG 1380 

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                     4600-0093.33
                                                                                                                              APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 209,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-CCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
          US 822,335
                                                                                                                                                                                                                                                        NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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INDIVIDUAL ISOLATE: ORF
US-07-876-941A-3
                         17-JAN-1992
          APPLICATION NUMBER: FILING DATE: 17-JAN
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                     Hepatitis E Virus (Burma strain)
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                                                                             100.0%; Score 1983;
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Best Local Similarity 100.
Matches 1983; Conservative
                  ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-542-634-1
    ORIGINAL SOURCE:
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                                                                                                                                                ATTICCACTIACACCACTAGCCTGGGTGCTCCCGTCTCCATTICTGCGGTTGCCGTT
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APPLICANT: McAtee, C. Patrick
APPLICANT: Arbough, Patrice O.
APPLICANT: Zhang, Yifan
TILE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR CORRESPONDENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEFANDE: (415) 324-0880
TELEFAX: (415) 324-0800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Dehlinger & Associates
350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-542-634-1; Sequence 1, Application US/08542634; Patent No. 6214970; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                      Sequence 1, Application US/08477292

Patent No. 6291641

GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas
APPLICANT: McMee, Patrick
APPLICANT: Yarbough, Patrick
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                      ADDRESSEE: Cathleen M. Desjardins, M. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/327,952
APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G32P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415)369-9500
TELEPAX: (415)368-0709
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
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Best Local Similarity
Matches 1983; Conserv
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US-08-477-292-1
RESULT 6
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   TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG
                    GGCGGCCTGCCGACAGAATTGATTTCGTCGCTGGTGGCCAGCTGTTCTACTCCCGTCCC
                                                                         CTCACCACCACGGCTGCTACCCGGCTTTATGAAGGACCTCTATTTACTAGTACTAATGGT
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                                                                                               GCTGTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCACGACG
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                                 481 AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 420,921
FILING DATE: 13-CTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
TELEPHONE (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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; INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain); INDIVIDUAL ISOLATE: ORF-2 PCT-US95-13703-1	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps 0	CGGCCTALTITGTIGCTGCTCCTCATGTTTTTGCCTATGCTGCCGG		QY         121 TTCTGGGGTGACCGGGTTGATTCTCAGCCTTGCAATCCCTATATTCATCCAACCAA			Qy         301 AGACCTACCACAGGGCGCGCGCCGCTAACGGGGTCGCTCCGGCCCATGACACCCGG         360           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         361 CCAGTGCCTGATGTCGACTCCCGCGGCGATCTTGCGCCGGCGGTATAACCTATCAACA 420           DD         361 CCAGTGCTGATGTCGACTCCCGCGGGCGCCATCTTGCGCCGGCGGTATAACCTATCAACA 420	QY         421 ICTCCCCTTACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCCTCTT 480           DD         421 ICTCCCCTTACCTCTTCCGTGGCCACCAGACTGGTTCTTATGCCGCCCCTCTT 480	QY         481 AGTCCGCTTTACCCCTTCAGGACGCCACCAATACCCATATAATGGCCACGGAAGCTTCT 540           Db         481 AGTCCGCTTTACCCCTTCAGGACGCCACCAATACCCATATAATGGCCACGGAAGCTTCT 540	Oy 541 AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCTGGTCCCCAAT 600	OY 601 GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCGGCG 660	Qy 661 TCCGTTGATATGAATACCACGGAGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720	Qy 721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATGGTAACCAAGGCTGGCGCTC 780	Qy 781 GTCGAGACTCTGGGGTGGCTGAGGAGGTACCTCTGGTCTTGTTATGCTTTGCATA 840  Db 781 GTCGAGACTCTCTGGGTGGCTGAGGAGGCTACCTCTGTTATGCTTTGCATA 840	OY 841 CATGGCTCACTCGTAAATTCCTATACACACCTATACCGGTGCCCTCGGGCTGTTG 900	QY         901 GACTITGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC 960	Qy 961 TCCCGTTATTCCAGCACTGCTCGCCACCGCTTCGTCGCGGTGCGGGACGGGACTGCCGAG 1020
OY 1561 CTIGACGGTCGCCCTCTCCACCATCCAGGAGTACTCGAAGACCTTCTTGTCCTGCCG 1620	Qy 1621 CTCCGCGGTAAGCTCTTTCTGGGAGGCAGCCACTAAAGCCGGGTACCCTTATAAT 1680 	QY         1681         TATAACACCACTGCTAGGGACCAACTGCTTGTCGAGATGCCGCGGGCACGGGTCGCT         1740           Db         1681         TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGGCACCGGGTCGCT         1740	OY 1741 ATTICCACTTACACTAGCCTGGGTGCTGGTCCCGTCTCCATTICTGCGGTTGCCGTT 1800	OY 1801 TTAGCCCCCACTCTGCGCTAGCATTGCTTGAGATACCTTGGACTACCCTGCCCGGGCC 1860	Qy         1861         CATACTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGCTGCGCTTTC         1920           Db         1861         CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGCTGCGCTTTC         1920	OY 1921 CAGTCTACTGTCGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 1980 	Qy 1981 TAG 1983           Db 1981 TAG 1983	RESULT 8 PCT-US95-13703-1 ; Sequence 1, Application PC/TUS9513703	; GENERAL INFORMATION: ; APPLICANT: ; TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND ; TITLE OF INVENTION: USES THEREFOR	; NUMBER OF SEQUENCES: 31 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Dehlinger & Associates ; STREET: P.O. Box 60850	; CITY: Palo Alto ; STATE: CA ; COUNTRY: USA ; ZIP: 94306-0850		<pre>SOFTWARE: PatentIn Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: PCT/US95/13703 ; FILING DATE:</pre>	AI	REFERENCE/DOCKET NUMBE TELECOMMUNICATION INFORM TELEPHONE: (415) 324-05 TELEFAX: (415) 324-05	<ul> <li>INFORMATION FOR SEQ ID NO: 1:</li> <li>SEQUENCE CHARACTERISTICS:</li> <li>LENGTH: 2049 base pairs</li> <li>TYPE: nucleic acid</li> </ul>	; STRANDEDNESS: double : TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) ; HYPOTHETICAL: NO	; ORIGINAL SOURCE:

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                                 GENERAL INFORMATION:

APPLICANT: Bradley, Daniel W.

APPLICANT: Twu, Jr.-Shin

APPLICANT: Twu, Jr.-Shin

APPLICANT: Twu, Jr.-Shin

APPLICANT: Twu, Albert W.

APPLICANT: Krawczynski, Krzysztof Z.

APPLICANT: Krawczynski, Krzysztof Z.

APPLICANT: Yarbough, Patrice D.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY DISC.
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
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INDIVIDUAL ISOLATE: BURMA SEQUENCE, FIGURE
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ive 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
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APPLICATION NUMBER: US 420,921
APPLICATION NUMBER: US 420,921
FILING APPLICATION DATA:
APPLICATION NUMBER: US 367,486
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APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
          Sequence 1, Application US/08259148A
Patent No. 5741490
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REGISTRATION WUMBER: 38,615
REPERENCE/DOCKET NUMBER: 4600.
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 324-080
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                    COMPUTER KEALDABLE FORM:
MEDIUM TYPE: FISIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 870,985
FILING DATE: 07-DAPRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 1-0-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 1-0-APRIL-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 1-0-CTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 1-0-CTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 1-0-TOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 1-0-TOBER-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
FELERENCE/DOCKET NUMBER: 4600-0093.38
TELERENCE/DOCKET NUMBER: 4600-0093.38
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEAFAX: ANG PASSE 
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BURMA SEQUENCE, FIGURE
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                                             3: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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Best Local Similarity 100.
Matches 1983; Conservative
                                         ADDERSEE: Dehlinger STREET: 350 Cambridge CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy d
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STRANDEDNESS: double
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US-08-484-054-1
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  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
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                                                                                                                                                                                                                                          APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY AGENT INFORMATION:
NAME: SHOLT, CHAILES K.
                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,615
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MOLECULE TYPE: CDNA to mRNA
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Matches 1983; Conservative
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INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: doub
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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Patent No. 5885768
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Mitchell, Carl
TITLE OF INVENTION: Hepatitis E Virus Per
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MEDIUM TYPE: Floppy disk
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BURMA SEQUENCE, FIGURE
US-07-870-985A-1
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100.0%; Score 1983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
                                                                                                                                                                                                                           NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ANDANE: MARKET INFORMATION:
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FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 17-JUN-1988
ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEPHONE: (650) 324-0880
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6: SEQUENCE GRARACTPERISTICS:
LENGTH: 7195 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HEV
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HYPOTHETICAL:
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; LOCATION:
US-08-478-507-6
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No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
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                                                                                                                                                                                                                                                                1846 TTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGGCCCGCGCC
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                                                                                                                                                  1741 ATTICCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
                                                                                                                                                                                                                                     1801 TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCC
                                                             1726 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
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MEDIUM TERRES FIORDS disk
COMPUTER: Floppy disk
MEDIUM TERRES Floppy disk
COMPUTER: Floppy disk
Floppy disk
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COMPUTER: Floppy disk
TLING DATE: CF-MUL-1994
FLING DATE: CF-MUL-1994
FILING DATE: CF-ME-1991
FILING DATE: CF-ME-1991
FILING DATE: CF-ME-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk B
TITLE OF INVENTION: DNA Sequences of
TITLE OF INVENTION: NO. 6120988-A/NO
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATION NUMBER: US 07/367,486
DATE: 16-JUN-1989
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APPLICATION NUMBER: US 07/336,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08478507
Patent No. 6120988
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FILING DATE: 16-JUN
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APPLICANT: Reyes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG 1983
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	REGULT 14  US-09-128-275A-6  IS-09-128-275A-6  Sequence 6, Application US/09128275A  Sequence 6, Application US/09128275A  Setter No. 6229005  SERVINGERAL INFORMATION: SERVINGERAL INFORMATION: APPLICANT: Reves. Gregory R  APPLICANT: Team, Albert  APPLICANT: Tam, Albert  APPLICANT: Pay O Albert  CITY: Pay O Albert  CONTWER: DATE OF UNWARION: Suite 250  CITY: Pay O Albert  CONTWER: DATE OF UNWARION: Suite 250  CITY: Pay O Albert  CONTWER: DATE OF UNWARION: PAY OF USE O
541 AATTATGCCCAGTACCGGGTTGCCCGTGCCAATCGTTACCGCCCGC	100

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                                                CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
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APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
ATTONEY/ABOTT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECHONNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6:
INFORMATION FOR SE
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100.0%; Score 1983;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1983; Conservative 0; Mismatches
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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28..5106
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NAME/KEY:
LOCATION:
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US-09-128-275A-6
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100.0%; Pred. No. 0;
tive 0; Mismatches
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APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                            NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7195 base pairs
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5106..5474
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STRANDEDNESS: double
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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ORIGINAL SOURCE
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LOCATION:
FEATURE:
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Matches 1983;
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Patent No. 6379891

GENERAL INFORMATION:
APPLICANT: Reversed Gregory R
APPLICANT: Bradley, Daniel W
APPLICANT: Tank Albert
APPLICANT: Tank Albert
APPLICANT: Tank Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                             6767 CTCCGCGGTAAGCTCTTTTTTTTTTTTTTAAAGCCACAACTAAAAGCCGGGTACCCTTATAAT
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                                                                                                                                                                                                                   6887 ATTICCACTIACACCACTAGCCTGGTGCTGGTCCCGTCTCCATTICTGCGGTTGCCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORKENT APPLICATION DATA:
PRICATION NUMBER: US/09/553,427
FILING DATE:
PRICATION NUMBER: US/08/478,507
FILING DATE: 07-UNN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-UUL-1994
PRICA APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-ARR-1991
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-ARR-1990
PRICA APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRICA APPLICATION NUMBER: US 07/505,888
FILING DATE: 13-0CT-1989
PRICA APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-0CT-1989
PRICA APPLICATION NUMBER: US 07/420,921
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 164, App Sequence 165, App Sequence 165, App Sequence 89, Appl Sequence 89, Appl Sequence 90, Appl Sequence 9, Appli Sequence 7, Appli Sequence 129, Appl Sequence 129, App Sequence 6, Appli Sequence 129, App Sequence 6, Appli Sequence 6, Appli Sequence 129, App Sequence 6, Appli Sequence 6, Appli

Sequence 193, App Sequence 196, App Sequence 193, App Sequence 196, App Sequence 192, App Sequence 192, App Sequence 195, App Sequence 195, App

Sequence 24, Sequence 24, Sequence

US-10-319-745-24

ALIGNMENTS

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APPLICANT: Fuerst, Thomas R.
APPLICANT: Fuerst, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: UDKNOWD>
US-10-239-090A-45
US-10-239-090A-11
US-10-239-090A-44
US-10-239-090A-44
US-209-468-147-164
US-209-468-147-165
US-209-468-147-165
US-209-468-147-89
US-209-769-066-4
US-209-769-066-4
US-209-769-066-4
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US-209-769-066-5
US-209-769-066-6
US-209-769-066-6
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US-10-319-745-195
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US-10-319-745-195
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/542,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09769066; Patent No. US20020107360A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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ZIP: 94306
COMPUTER READABLE FORM:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-165-868-3

US-10-165-868-1

US-09-851-410-6

US-10-381-770-5

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US-09-769-066-3

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Gapop 10.0 , Gapext 1.0
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        GACTITGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACAATACGCGGGTC
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: Hepatitis
                                                        ORF-2
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1-09-769-066-1
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Best Local Similarity 100.0%;
Matches 1983; Conservative 0
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APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr.Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Met
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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SEQUENCE DESCRIPTION: SEQ ID
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LENGTH: 2049 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                        Sequence 3, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
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                                                     TAG 1983
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US-10-165-868-3
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Length 2049;

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100.0%; Score 1983;

Query Match

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                                                   Tam. Albert W.

Krawczynski, Krzysztof Z.

Krawczynski, Krzysztof Z.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS: 24

ADDRESSE: 25

STREET: 350 Cambridge Avenue, Suite 250

STREET: 350 Cambridge Avenue, Suite 250
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-165-868-1
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PILING DATE: 20-APRIL-1992

PELLING DATE: 20-APRIL-1992

PELLING DATE: 17-JAN-1992

PELLING DATE: 17-JAN-1992

APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

APPLICATION NUMBER: US 420,921

FILING DATE: 13-OCTOBER-1989

APPLICATION NUMBER: US 367,486

FILING DATE: 11-APRIL-1989

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

APPLICATION NUMBER: US 208,997

FILING DATE: 17-JUNE-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, GATY R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 4600-0093.30

TELECOMMUNICATION INDERER: 33
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100.0%; Pred. No. 0;
ive 0; Mismatches
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APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
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Best Local Similarity
Matches 1983; Conserv
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                                   GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                            GTCGGTGAGATCGGCCGCGGGGATAGCCCTCACCTGTTCAACCTTGCTGACGTTCGCTG
                                                                                                              GGCGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC
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Page 5

OY 1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320	Qy 1321 CAGGATTATGATAACCAACATGAACAAGATCGGCGGACGCCTTCTCCAGCCCATCGCGC 1380	QY 1381 CCTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCCACCGCTGCCGAGTAT 1440	OY 1441 GACCACTCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 1500	Oy 1501 GTTAATGTTGCGACCGGGGCGTGGTTGCCGGTCGCTTGGACCAAGGTCACA 1560	Qy 1561 CTTGACGCTCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCG 1620	Oy         1621         CTCCGCGGTAAGCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT         1680           Db         1666         CTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAAT         1725	Qy         1681         TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCT         1740           Db         1726         TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT         1785	Qy         1741 ATTICACTTACACCACAGACCTGGGGCTGCCCGTCTCCATTCTGCGGTTGCCGTT 1800           Db         1786 ATTICCACTTACACCACAGGCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 1845	Ay 1801 TIAGCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGGCC 1860	OY 1861 CATACTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC 1920	OY 1921 CAGICTACTGTCGCTCAGCCTTCAGCGCCTTAAGATCAAGGTGGGTAAAACTCGGGAGTTG 1980  1966 CAGICTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 2025	OY 1981 TAG 1983           Db 2026 TAG 2028	RESULT 4 US-09-851-410-6 ; Sequence 6, Application US/09851410	Publication No. GENERAL INFOR APPLICAN	; TITLE OF INVENTION: DNA Sequences of Enterically Transmitted ; NO. US20030124510Al-A/No. US20030124510Al-B Hepatitis Viral ; CORRESPONDENCE ADDRESS:	
CTTCGCCCCCGARGTCACCGCTGCGGCCGGGGCTGGACCTCGTGTTCGCCAACCCGCC 240		GACCTACCACAGCTGGGGCGCGCGCTAACCGCGGTCGGCTCCGGCCCATGACACCCCG			SCTITIACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT	CCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC	GOGGITACGCCATCTCCATTCTGGCCACAGACCACCACCACCGCGGGG 66	ACCTCGACGGAIGTTCGTATTTTAGTCCAGCCGGCATA 72	AGCTGGCGCTCC 78	ATA 84	GGTAAATTCCTATACTAATACACCCTATACGGTGCCCTCGGGTGTGTTG 90	CCTTGAGCTTGAGTTTCGCAACCTTACCCCGGTAACACCAATACGCGGGTC 96	CCCGTTATTCCAGGACTGCTCGCCACGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020		120	(n —

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                                                           Version #1.25
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                                                                                                                                                                                                                                                                                                                                               NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
                                                                                                                                           FILING DATE: «Unknown»
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/336,F72
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/308,997
FILING DATE: 11-APR-1988
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  COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDBY disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,410
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                                                                                                                                 APPLICATION NUMBER: 09/128,275
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                      3; (650) 324-0880
(650) 324-0960
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TELEPHONE: (650) 324-0880
                                                                                                    FILING DATE: 07-May-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 7195 base pairs
TYPE: nucleic acid
STRANDEDNESS: HEV - Burm
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28..5106
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
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Best Local Similarity 100.
Matches 1983; Conservative
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6467 1381 6527 1441 6587 6647	162 676 168 682	6827 TATAACACCACTGCTAGCACCTGGCTGGCTGGCTGGCTGG	CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGCGCTGCC CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCCTTGGCCTTCAGGCTGCC CATACTTTTGATATTTCTGCCCCAGAGTGCCGCCCCTTTGGCCTTCAGGCTGCC CAGTCTACTGTGCGCTGAGCTTCAGGCCTTAAGATGAAGGTGCGTAAAAACTCGGC CAGTCTACTGCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGC CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGC	y 1981 TAG 1983 b 7127 TAG 7129 ESULT 5	; Sequence, 5. Application No. US20040052813A1; GENERAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: YANG STRING TANG company, Ltd. ; TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS; TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS ; FILE REPREBENCE: IECO10037PCT ; CURRENT APPLICATION NUMBER: US(10/381,770 ; CURRENT FILING DATE: 2003-07-16		Ouery Match  Best Local Similarity 94.4%; Pred. No. 0;  Matches 1872; Conservative 0; Mismatches 111; Indels 0; Gaps 0;  Oy 1 ATGCGCCTCGGCCTATTTGTTGCTCTCATGTTTTTGCCTATGCTGCCGGCCA 60

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GACTITGCCCITGAGCTIGAGITTCGCAACCITACCCCCGGTAACACACAATACGCGGGIC 960
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                                                                         Score 1793.4;
Pred. No. 0;
0; Mismatches
                                                                           Query Match 90.4%;
Best Local Similarity 94.4%;
Matches 1871; Conservative (
                                                 virus
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version
SEQ ID NO 6
LENGTH: 1989
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                                       TYPE: DNA
CORGANISM: hepatitis
US-10-381-770-6
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TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE
TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILLE REPERBECE: IECO10037PCT
CURRENT APPLICATION UNDHER: US/10/381,770
CURRENT APPLICATION UNDHER: US/10/381,770
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                                                               CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTTATT
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                          GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
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Publication No. US20040052813A1
GENERAL INFORMATION:
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TITLE OF INVENTION: **LEARTH TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STRIE: CA
COUNTRY: USA
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WINDLIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
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FIGURE 2
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 0;
tive 0; Mismatches
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CLASSIFICATION: <Unknown>
                                                                                                 Sequence 3, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
MCAtee, C. Patrick
Yarbough, Patrice (
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TELEFAX: (415) 324-0960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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STRANDEDNESS: double
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Matches 1647; Conservative
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1 01 01	61 CCGCCCGGTCAGCCGTCTGGCCGCCGCGCGCGCGCGCGGTTCCGGCCGCTGGT 120	121 TTCTGGGGTGACCGGGTTGATTCTCAGCCTTCGCAATCCCTATATTCATCCAACCAA	241 GACCACTCGGCTCGGCTTGGCGTGACCAGGCCCAGCGCCCGCC		TCTCCCCTTACCTCTTCCGTGGCCACCGGGCTTACACTCGTTCTTATGCCGCCTCTT 48	481 AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540	CCAAT       CTAAT	601 GCTGTCGGCGGTTACGCCATCTCCATCTGGCCACAGACCACCACCACCGACG 660	661 TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720					961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGGACTGCCGAG 1020

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                                                               APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Ur-Shin
Purdy, Michael A.
Tam, Albert W.
Traw. Traw. Yrzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILLING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 622,335
FILLING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILLING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILLING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                  ADDRESSE: Delinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
STATE: CA
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Pred. No. 0;
0; Mismatches
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APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
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STRANDEDNESS: double
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Best Local Similarity 81.0%;
Matches 1606; Conservative
                  US20030143241A1
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                            GENERAL INFORMATION:
                     Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-165-868-4
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Pred. No. 0;
0; Mismatches 374; Indels
                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/870,985A FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 10-UNBER: US 367,486
FILING DATE: 11-AUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,869
FILING DATE: 06-Jun-2002
CLASSIFICATION: ¢Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324-0960
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MOLECULE TYPE: CDNA to mRNA
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STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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81.0%;
                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
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Publication No. US20030143241A1

GENERAL INFORMATION:

APPLICANT: Reyes, Gregory R.

Twu, Jr-Shin

Purdy, Michael A.

Tam, Albert W.

Krawczynski, Krzysztof Z.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
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1441 GACCAGTCCACTTATGGCTCAGATTATGTTTTCTGACTCTGACCTTG 1500	RESULT 11  US.09-811-410-10  Sequence 10, Application US/09851410  Sequence 10. Application No. US20030124510A1  Publication No. US20030124510A1  GENERAL INFORMATION: Reves, Gregory R  Yarbough, Partice O  Bradley, Daniel W  Krawczynski, Krzysztof Z  Tum, Albert  Fry, Kirk E  TITLE OF INVENTION: DNA Sequences of Enterically Transmitted  NUMBER OF SEQUENCES: 20  CORRESPONDENCE ADDRESS: 20  CORRESPONDENCE ADDRESS: 20  CORRESPONDENCE ADDRESS: 20  CORPEREST: 350 Cambridge Avenue, Suite 250  CITY: Palo Alto  STREET: 350 Cambridge Avenue, Suite 250  CITY: Palo Alto  STREET: BP Alto  COMPUTER READABLE FORM:  MEDIUM TYPE: 10497 disk  COMPUTER: IMP PC Compatible  COMPUTER: IMP PC Compatible  COMPUTER: BP PC Compatible  COMPUTER: STATE: P2306  CURRENT APPLICATION DATA: SC99/851,410  FILING DATE: 07-484-2001  PRIOR APPLICATION DATA:  PRIOR APPLICATION DATA:  APPLICATION NUMBER: 09/128,275
346 CGACCTGCCACAGCCGGGCTGACGGCTGTGGCGCCCATGACATACACTACAAAAAAACCTGCACAGCCCACATACAAAAAAAA	961 TCCCGTTATTCCAGCACTGCTCGCCCCTTCGTCGCGGTGCGGACTGCCGAG 1020

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FILING DATE: <Unknown>
FILING DATE: <Unknown>
FILING DATE: OS-APR-1991
APPLICATION NUMBER: US 07/505,888
FILING DATE: OS-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-OCT-1989
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
NAME: PEFIL HORY, JOANNER: 4600-0183.24
TELEROMMUNICATION INFORMATION:
FILERPHORE (650) 324-0880
TELERPHORE (650) 324-0860
INFORMATION FOR SEQ ID NO: 10:
SEQUENA: 7771, PAGE 2015
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TYPE: nucleic acid
STRANDEDNESS: Composite Mexico strain
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ANTI-SENSE: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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81.0%;
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Matches 1606; Conservative
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	RESULT 13 US-10-239-090A-48 Sequence 48 Application US/10239090A Publication No. US20040101820A1 GENERAL INFORMATION TITLE OF INVENTION: Polynucleotide probe and primer derived from hepatitis E virus con TITLE OF INVENTION: Etom Japanese, chip including the same, kit including the same, TITLE OF INVENTION UNDERS. US/10/239,090A TITLE OF INVENTION OF ETOM TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN

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                                                                        TYPE: DNA
ORGANISM: Hepatitis B Virus Japan JKK-Sap(AB074917)
                                                                                                                                                                           394;
                                                                                                                                        Score 1347.6;
Pred. No. 0;
                                                                                                                                                                             0; Mismatches
                                                                                                                                        Query Match 68.0%;
Best Local Similarity 80.1%;
Matches 1584; Conservative
 2001-06-25
PRIOR FILING DATE: 200
NUMBER OF SEQ ID NOS:
SEQ ID NO 47
                                                                                              , ORGANISM: Hep
US-10-239-090A-47
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Sequence 47, Application US/10239090A
Bublication No. US20040101820A1
GENERAL INFORMATION:
APPLICANT: KABUSHIKI KAISHA TOSHIBA
APPLICANT: KABUSHIKI KAISHA TOSHIBA
TITLE OF INVENTION: Polynucleotide probe and primer derived from hepatitis E virus or
TITLE OF INVENTION: from Japanese, chip including the same,
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REFERENCE: 0280741P
CURRENT APPLICATION NUMBER: US/10/239,090A
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: JP2001-191837
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US-10-239-090A-45

Sequence 45, Application US/10239090A

Sequence 45, Application US/10239090A

Publication NO. USZ0040101820A1

GENERAL INFORMATION:

APPLICANT: KABUSHIKI KAISHA TOSHIBA

TITLE OF INVENTION: From Japanese, chip including the same,

TITLE OF INVENTION: detecting hepatitis E virus using the same

TITLE OF INVENTION: detecting hepatitis E virus using the same

CURRENT APPLICATION NUMBER: US/10/239,090A

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: J2001-191837

NUMBER OF SEQ ID NOS: 57

SEQ ID NO 45

LENGTH: 7233
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80.0%; Pred. No. 0;
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ORGANISM: Hepatitis E Virus Japan JMY-Haw(AB074920)
10-239-090A-45
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                                                                                                                                                                                                                                                                                                                                                                                        SPGHEWRSANPFCGESTLYTRYWSTITDTPLTVGLISGHLDAAPHSGGPPATGRAV
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                                                                                                                                                                                                                                                                                                      TAEPATLDITGSYIVDGRSLQTVYQALDLPADLVARAARLSATVTVTETSGRLDCQTM
IGNKTFLTTFVDGARLEVNGPEQLNLSFDSQQCSMAAGPFCLTYAAVDGGLEVHFSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOKDCNKFTTGETIAHGKVGQGIFRWSKTFCALFGPWFRAIEKAILSLLPQAVFYGDA
YDDSVFSAAVAGASHAMVFENDFSEFDSTQNNFSLGLECAIMEECGMPQMLVRLYHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAWILLQAPKESLRGFWKKHSGEPGSLLWNTVWNMAIIAHCYEFRDLQVAAFKGDDSV
VLCSEYRQSPGAGSLIAGCGLKLKADFRPIGLYAGVVVAPGLGALPDVVRFAGRLSEK
NWGPDPERAEQLRLAVQDFLRRLTNVAQICVEVVSRVYGVSPGLVHNLIGMLQTIGDG
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GHTDVRASLARFIPTLGRVTATTCELFELVEAMVEKGQDGSAVLELDLCSRDVSRITF
                                                                                                                                                          VTYEGDTSAGYNHDVATLRTWIRTTKVVGEHPLVIERVRGIGCHFVLLITAAPEPSPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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AGCAG	Matches 1644;	
	Db CTGTGGGCCTGCCCATGACACCTCACCGGAGGTGATTGAT	GGACGTTGATTCTCGCGGTGCAATT 393 
1321 GATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCT 1380 	QY 394 CTACGCCGCAGTATAATTTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT	3ACATCCTCTGTGGCCTCTGGCACT 453
1381 TITICTGTTCTCCGAGCAAATGATGTACTTTGGCTGTCCCTCACTGCAGCGGTTTGAG 1440	Qy 454 AATTTAGTCCTGTATGCCGCCCCCTTAATCCGCCTCTGCGCTGCAGGACGGTACTAAT	51
1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG 1500	QY         514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACGGGTTGCCGGCGTACT           Db         181 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACGGGGTTGCCGGGGTTATGCACAGTACGGGGTTGCCCGGGGTTATGCACAGTACGGGGTTGCCCGGGGTTATTATGCACAGTACGGGGTTGCCCGGGGTTATTATTATGCACAGTACCGGGGTTGCCCGGGGTTATTATTATTATTATGCACAGTACCGGGGTTATGCACAGTACCGGGGTTATTATTATTATTATTATTATTATTATTATTATTA	N 0
1501 AATGTTGCGACTGGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTC 1560 	QY 574 ATCCGTTACCGGCCCTAGTGCCTAATGCAGTTGGAGGCTATGCTATATCCATTTCTTTTTTTT	30 30
1561 GACGGGCGCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTGTGCTCCCCCTT 1620 	Qy 634 TGGCCTCAAACAACCACAACTGTTGACATGAATTCCATTACTTCCACTGAT 	3 6
1621 CGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAAAAGCAGGTTATCCTTATAATTAT 1680 	Qy 694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCG	
1681 AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT 1740 	Qy         754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAAGCC           Db         421 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGAACATCTGGTTTGCTGAGGAAGCC	81 48
1741 TCAACCTATACCACCCTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGGGTTTTG 1800 	Qy 814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACCAAAAACCAB	87 54
1801 GCTCCACGCTCCGCCCTGGTTGCTGAAGATACTTTTGATTATCCGGGGCGGCGCAC 1860 	Qy 874 CCTTAIACGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGGCAATCTC 	TTAGAGCTTGAGTTTCGCAATCTC 933 
1861 ACAITTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG 1920 	Qy         934 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGGACTGCTCGTCACCTCCTCGGCC           Db         601 ACCACCTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTCCTCGTCACTCCGCC	TCCAGCACTGCTCGTCACTCCGCC 993
1921 TCAACTGTCGCTGAGCTCCAGGGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 1980 	Qy 994 CGAGGGCCGACGGCTGCGGAGCTGACCACAACTGCAGCCACCAGGTTCATGAAGAT 	
RESULT 11 AR170407 LOCUS LOCUS DEFINITION Sequence 4 from patent US 6291641. ACCESSION AR170407 ACESSION AR170407.1 GI:17908366	QY         1054 CTCCACTTTACCGGCCTTAATGGGTGAAGTCGGCCGGGGATAGCTCTAACATTA	GGCCGCGGGATAGCTCTAACATTA 1113  [
_	Qy 1174 GGGCAACTGTTTATTCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACGGT 	12
AUTHORS Fuerst, T.R., McAtee, C. Patrick., Yarbough, P.O. and Zhang, YF. TITLE Hepatitis E virus antigens and uses therefor JOHNAL Patent: US 6291641-A 4 18-SEP-2001; FEATURES Location/Oualifiers	QY     1234     TATACATCAGTGGAGAATGCTCAGCAGGATAAGGGTGTTGCTATCCCCCCACGATATCGAT       Db     901     TATACATCAGTGGAGAATGCTCAGCAGATAAGGGTGTTGCTATCCCCCACGATATCGAT	12
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Query Match 83.0%; Score 1644; DB 6; Length 1644; Best Local Similarity 100.0%; Pred. No. 0;	QY     1354     ACCCGGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGGAAATGATGTACTTTGG       Db     1021     ACCCGTCGCCTGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTTTGG	CTCCGAGCAAATGATGTACTTTGG 1413 

FEATURES Location/Qualifiers source 11983 /organism="unidentified" /mol_type="genomic DNA" /db xref="taxon.3544"	atch 69.6%; Score 1378.2; DB 6; Length 1983; cal Similarity 81.3%; Pred. No. 0;	valive       0;       Mismatches       368;       Indels       3;         AGGCCTCTTTTGTGCTGCCTATGTTGCCCG       111111111111111111111111111111111111	Db 1 Arcidecercadecerafrirjarjacricercardifrirateceraterradecegeed 60  Qy 61 ccaaccegercadecegeecegeegeegegegegegegegegegegegegeg	Db 61 Cdaccddrafacddrafaeddrafaeddaeddaeddaeddaeddaeddaeddaeddaeddae		Db 181 CCCTTCGCCCCGATGTCACCGCTGCGGGCTGGGGCTGGACCTCGTGTTCGCCTAACCAGCC 240  Qy 241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGGCCCCTCCGCTGCCTCCGTGC 300	Db 241 daAccacacacacacacacacacacacacacacacacaca		Db 361 CCAGTGACTGACTCTGGGGGGCCATCTTGGGCGGGGATATAATCTATCAACA 420  Qy	481 481 541 601 661 721 721 781 781 841
Oy         1414         CTGTCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTT         1473           Db         1081         CTGTCCCTCACTGCAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTT         1140	CCCGA 	Qy 1534 TCGCTTGACTGGTCCAAGTCACCCTCGACGGCCCCTCCCGACTGTTGAGCAATAT 1593  1201 TCGCTTGACTGGTCCAAGTCACCCTCGAGGGGCCCCTCCCGACTGTTGAGCAATAT 1260	Qy         1594         TCCAAGACATCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACA         1653           Db         1261         TCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACA         1320	Qy         1654         ACABABAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGATTGAT	OY 1714 AATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACGGGTTGGGGCCGGTCG 1773	Oy 1774 GTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGGGAT 1833	Qy         1834         ACTITIGATIANCCGGGCGCGCACACALITGATGACTICCCCCTGAATGCCGCGCT         1893           Db         1501         ACTITIGATIANCCGGGCGCGCACACATITGATGACTICTGCCCTGAATGCCGCGCT         1560	Oy 1894 TTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTT 1953	Oy 1954 AAGGTGGGTAAAACTCGGGAGTTG 1977 	RESULT 12   B17107   B1711790   B17107   B1711790   B17107   B17

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TYEGDTSAGYNHDVSNLRSWIRTTKVTGDHPLVIERVRAIGCHFVLLLTAAPEBSEMP
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F117 . 7099
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                                                                                                                                                   VRL 02-AUG-1993
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CCSRLMTYLRGI SYKVTVGTLVANEGWNASEDALTAVITAAYLTICHQRYLRTQAISK
GMRRLEREHAQKFI TRLYSWLFEKSGRDYI PGRQLEFYAQCRRWLSAGFHLDPRVLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELEQGLLYLPQELTTCDSVVTFELTDIVHCRMAAPSQRKAVLSTLVGRYGRRTKLYN
ASHSDVRDSLARFIPAIGPVQVTTCELYELVEAMVEKGQDGSAVLELDLCSRDVSRIT
FFQKDCNKFTTGETIAHGKVGQGISAMSKTFCALFGPWFRAIEKAILALLPQGVFYGD
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IVLCSEYRQSPGAAVLIAGCGLKLKVDFRPIGLYAGVVVAPGLGALPDVVRFAGRLTE
KNWGPGPERAEQLRLAVSDFLRKLTNVAQMCVDVVSRVYGVSPGLVHNLIGMLQAVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFDDTVFSAAVAAAKASMVFENDFSEFDSTQNNFSLGLECAIMEECGMPQWLIRLYHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsarev,S.A., Emerson,S.U., Reyes,G.R., Tsareva,T.S., Legters,L.J., Malik,I.A., Iqbal,M. and Purcell,R.H.
Malik,I.A., Iqbal,M. and Purcell,R.H.
Pharacterization of a prototype strain of hepatitis E virus
Proc. Natl. Acad. Sci. U.S.A. 89 (2), 559-563 (1992)
92115700
                                                                                                                                                                                                                                                                                                              Hepatitis E virus
Hepatitis E virus
Viruses; ssRMA positive-strand viruses, no DNA stage; Hepatitis
E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source text: Hepatitis E virus (strain SAR-55) cDNA
                                                                                                                                            7138 bp ds-RNA Hepatitis E Virus, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Hepatitis E virus"
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	RESULT 14  AR139826  LOCUS  DEFINITION Sequence 4 from patent US 6207416.  AR139826  AR13982  AR148232  AR168A  AR148A  AR148A  AR148A  AR148A  AR148A  AR16A  AR148A  AR148A  A	OBJUSTANCE   CONTRICTOR   CON

5447	Db 5507 CCAGTGCTGATTGATTCTCCGGGGGGCGCTCCTGGGGGGGG	Qy 421 TCACCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTTTDCTTTAGTCTGTTTTAGTTTTAGTCTTTTACGCCGCTCCTTTTTTTT	OY 481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC	541	Qy         601 GCAGTTGGAGGCTATGCTATATCCATTTCTTTCTGGCCTCAAACAACCACACACCACACACA	5807	Qy 721 GCATCTGAATTGGTCATCCCAAGGGGCCTTCACTACCGCAATCAAGGTTGGCGCTCG	Qy 781 GITGAGACATCIGGIGITGCTGAGGAAGCCACCICCGGICTIGICAIGITAIGCAIA	Qy 841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACGGTGCCCTTAGGCTTACTG  5987 CATGGCTCACCTGTAAATTCTTATACTAATACACCCTATACGGTGCCCTCGGGCTGTTG	Qy 901 GACTTTGCCTTAGAGCTTTGAGTTTCGCAATCTCACCACCTGTAACACCCAATACACGTGTG	Qy         961 TCCGGTTACTCCAGCACTGCTCGTCAGCCCGAGGGCCGACGGACTGCGGGAG           Db         6107 TCGCGTTACTCCAGCACTGCCGTCACCGCCTTCGTCGTGGCGAGATGGGACTGCCGAG	Oy 1018 CTGACCACACAGGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGG	QY 1078 GTAGGTGAAGTCGGCGGGGGATAGCTCTAACATTACTTAACCTTGCTGACACGCTCCTC	Qy 1138 GGGGGGTCCCGACAGAATTATTCGTCGGCTGGCGGGCAACTGTTTATTCCCGCCGGCCG	Oy 1198 GTTGTCTCAGCCAATGGGGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAG	OY 1258 CACGATAAGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTGTCATTGTGATTCGCGTGTGGTCATTGTCATTGTATTGTATTGCAATCCCGCATGACATCGACTCGGGGGAATCCCGTGTAGTATTGTATTGTAATCCCGCATGACATCGACTCGGGGGAATCCCGTGTAGTATTTTTTTT	Qy 1318 CAGGATTATGACAACCAGCATGAGGATCGGCCCACCCGTGCGCCATCTCGG
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Hepatitis E virus; Burma; Mexico; immunoassay; peptide antigen; antibody; diagnosis; HEV; ds.
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                                                        A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen, and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence encodes the protein from the open reading frame, ORP2, from HEV Mexico strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS
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Best Local Similarity 100.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - are from the ORF1, against HEV infection.
TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAAGGTGGGTAAAACTCGGGAGTTGTAG
                         TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGGAGTTGTAG
                                                                                                                                                                 SS.
                                                                                                                                                                hepatitis; ET-NANB; vaccine;
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cive 0; Mismatches
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The sequence from a Mexican strain of ET-NAMB virus is about 75 per cent identical to the ETI.1 sequence (see AAQ14410). The Mexican sequence was identified in a cDNA library made directly from a semi-purified human stool specimen collected from an outbreak of ET-NAMB in Telixtac. Screening was with a serum considered to have high titer anti-ET-NANB antibodies. Two closes were identified from a total of 60,000 screened. The sequence of these clones was subsequently localised to the 3' half of the viral genome by homology comparison to the Burma strain sequence (see AAQ14412). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-field.)
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                                                                   Composite sequence from Mexican isolate of ET-NANB virus,
                                                                                                    non-A, non-B hepatitis virus;
deposit number 67717; Mexico;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                 90US-00505888
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                                    (first entry)
                                                                                                      enterically transmitted
E.coli strain BB4; ATCC
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                    (revised)
                                                                                                                                                                           hepatitis virus.
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25-MAR-2003
16-JAN-1992
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                                                                                                                                      The present sequence represents the composite Mexico strain sequence of enterically transmitted non A non B hepatitis virus (ETTANB) (hepatitis sequence) E virus (HEV). The specification describes an isolated protein which is specifically immunoreactive with antibodies present in individuals infected with HEV and encoded by a sequence contained in an open reading frame (ORF) of an HEV genome. The genome has a sequence that is more than 70% identical to the ORF1 sequence from Burma HEV isolate (AAV66321). The protein is used as a vaccine and a diagnostic probe for ET-NANB. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 27-AUG-2003 to correct of field.)
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                                              Hepatitis E virus proteins - useful for the virus.
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Best Local Similarity 100.0%;
Matches 1980; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonA/nonB hepatitis virus; identification; HEV;
TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGGAGTTGTAG
                                                               ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG
                                                                                                  ACATTTGATGACTTCTGCCCTCAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG
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100.0%; Pred. No. 0;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterically transmitted nonA/nor ET-NANB; detection; vaccine; ds
                                                                                                                                                                                                                                                                                   AAVS4730 standard; cDNA; 7171
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89US-00336672.
89US-00367486.
8US-00420921.
90US-00505888.
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Best Local Similarity 100.
Matches 1980; Conservative
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11-APR-1989;
19-JUN-1989;
13-OCT-1989;
05-APR-1990;
05-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-1994;
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The present invention describes a method for identifying a recombinant antigen immunoreactive with a hepatitis E virus (HEV)-induced antibody. The method comprises producing a polypeptide derived from an HEV genome, immunoreacting the polypeptide with an HEV-positive antiserum and selecting the polypeptide with an HEV-positive antiserum and selecting the polypeptide with an HEV-positive antiserum. The method is useful for reacts with the HEV-positive antiserum. The method is useful for identifying recombinant antigen immunoreactive with antibody induced by HEV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also known as HEV))-specific fragments are useful for identifying ET-NANB.

CC Known as HEV)-specific fragments are useful for identifying ET-NANB with genomic material in a patient sample, for the synthesis of polypeptides for use in immunoassays, and for identifying synthesis of polypeptides for use in immunoassays, and for identifying strain. The antiqens are especially useful in the preparation of vaccine against ET-NANB virus particles for use directly as antiviral agents, and to produce antiserum designed for pre- or post-exposure prophylaxis. The present sequence represente a specifically claimed HEV composite Mexican strain gene sequence for use in the present invention
                                                                                                                                                                                                                                                                                                                     Identifying recombinant antigen immunoreactive with antibody induced Depatitis E virus (HEV), for detecting HEV infection, comprises immunoreacting a polypeptide from an HEV genome with an HEV-positive
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Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein; immunological; diagnosis; hepatitis; infection; identification; detection; immunoreactive; hepatotropic; antiinflammatory; virucide; vaccine; antiviral; antigenic; antibody; antigen; ds.

Hepatitis E virus

JS6120988-A 19-SEP-2000

Hepatitis E virus Mexican strain nucleotide sequence SEQ ID NO:10.

(first entry)

AAA99260;

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1411   CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATATCTCGGACAGCGTGACTTTGGTG   1500	RESULT 7  AAR81496  ID AAR81486  ID AAR81486
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                                                                                                     The invention relates to an isolated DNA comprising the genome of an enterically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also preferred as HBV). The DNA sequences or their fragments are useful in preparing ET-NANB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The present sequence represents a Mexican strain composite ET-NANB viral
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                             New DNA sequences of enterically transmitted non-A/non-B (ET-NANB) hepatitis viral agent, useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
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                                                                                  Disclosure, Col 69-76; 45pp; English.
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Matches 1980; Conservative 0
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The invention comprises a method for detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a sample and isolating HEV agents or nucleic acid fragments produced by the agent. The method utilises PCR - using bile from a human or cynomolgus monkey actively infected with HEV as a source of the agent. The method of the invention is used for detecting the presence of a viral agent in a sample of cultured cells infected with the agent and isolating enterically transmitted nonA/nonB HEV agents or nucleic acid fragments produced by the agent. The present DNA sequence was isolated from a Mexican strain of the Hepatitis E virus
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monkeys using
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89US-00420921.
90US-00505888.
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
05-APR-1990;
15-APR-1991;
25-JUL-1994;
07-JUN-1995;
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The invention relates to a protein derived from an enterically transmitted non-A/non-B viral hepatitis agent. The viral proteins are useful for detecting infection by the enterically transmitted non-A/non-B (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for producing vaccines for immunising an individual against HEV hepatitis viral agent. The DNA fragments are useful for identifying and sequencing the entire viral agent and for assaying the viral agent in an infected sample. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis viral agent.
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                                                                                    88US-00208997.
89US-0035672.
89US-00367486.
89US-00420921.
9US-00505888.
91US-0061078.
94US-00128275.
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11-APR-1989;
16-JUN-1989;
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25-JUL-1994;
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	Score 1980; DB 9; Length 7180; Pred. No. 0; 0: Mismatches 0: Indels 0; Gaps 0;	TGCTGTTGTTCCTCTTGTTTCTGCCTAGTTGCCCGCCCA 60		180 5296	AGCC 240	rcgc 300       CGC 5416	360 5476		480 5596	CTCC 540       CTCC 5656	600 5716	660	720	CTCG 780	840 5956	900	ν.	1020 6136

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                                         block;
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                                         antibodies; infection;
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Pred. No. 0;
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                                      vaccine; neutralising; antibodies; ss.
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                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENELABS TECHNOLOGIES INC
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0
            and ORF3
                                                      open reading frame; antibodies;
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/*tag= a
/note= "ORF2"
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P-PSDB; AAR39307, AAR39308.
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          strain HEV
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Matches 1979; Conser
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20-APR-1992;
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GITGAGACATCTGGTGTTGCTGAGGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATA 840
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reagents for determining HEV infection and in vaccines
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Pred. No. 0;
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                           Disclosure, Page 71-72; 125pp; English
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                                                                                                                                                                                     CGTGGCAAGCTCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT
                             CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
                                                    CAGICCACITACGGGICGICAACIGGCCCGGITITAIAICICGGACAGCGIGACITIGGIG
                                                                               AATGTTGCGACTGGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCTTC
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Previously possible   Sequence 1983 BP; 342 A; 665 C; 485 G; 491 T; 0 U; 0 Other;   G9.6%; Score 1378.2; DB 2; Length 1983;   Best Local Similarity 81.3%; Pred. No. 0;   Matches 1612; Conservative 0; Mismatches 368; Indels 3; Gaps   ATGCGCCTAGGTCTTTTGCTGTTGTTTTCGCTAGTTTGCCGGCCA 60	GTGGT CCAAC CCAAC CAGCC CAGCC CAGCC	241 CGACCACTCGGCTTGGCTGACCAGCGCCCCGCCGCGCTGCTCCCAGCGCCCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGC	Db 361 CCAGTGCCTGATGTCGACTCTCGCGCCATCTTGCGCCGGCAGTATAATCTATCAACA 420  Qy 421 TCACCCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCCCCCTT 480	541 AATTATGCACAGTACCGGGTGCCTACTATCGTTACCGCCCCTAGTGCCTAT  [	Oy 661 TCTGTTGATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCACCTGGCATA 720	Db 781 Gredadcreteggegregergaggergaggerretegretegreteg

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Gaps

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368;

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                                                                                                                                                                                                                                                                                      /label= ORF-3 (AAR91815)
/notes="10" bp nucleic acid sequence TGGTNTTYGA has to be inserted between nucleotides 4390. .4391 for numbering to conform to that given in the specification"
                                                                                                                                                                                                                  /transl_except= pos:3739. .3741, aa:Glu
/note= "IO bp nucleic acid sequence TGGTNTTYGA has to binserted between nucleotides 4390. .4391 for numbering conform to that given in the specification"
                                                                                                    E virus, HEV, SAR-55 strain; enteric transmission, region; antigen; detection; antibody; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated and purified hepatitis E virus strain SAR-55 DNA - encoò antigenic protein useful in diagnosis, prophylaxis and treatment hepatitis E virus infection.
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                                                                               Hepatitis E virus strain SAR-55 cDNA (ATCC 75302)
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/label= ORF-1 (AAR91813)
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6157 CTCACCACCACGGCTGCTACTGGTTCATGAAGGACCTCTATTTACTAGTACTAATGGT 6216 1078 GTAGGTGAAGTCGGCGGGGGATAGCTCTAACTTAACCTTGCTGACGCTCCTC 1137	SCHOOL	6397 CAGGATAAGGGTATTGCAATGCCCCAACCCCGCGGGAATCCCGTCTAGTTATT 6456  1318 CAGGATTATGACAACCAGCATGACCACCCCCCCCCCCCC	1438   GACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTG	1558 CTCGACGGCCCCTCCCGACTGTTGACAATATTCCAAGACATTCTTGTGCTCCC	1678 TATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCC	1798 TTGGCTCCACGCTCGGCTCTGCTGCAGGATACTTTTGATTATCCGGGCGGG	1918 CAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTAAAACTCGGGAGTTG 1977  1057 CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTA 7116  1058 TAG 1980  117 TAG 119
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Search completed: August 21, 2004, 11:00:19 Job time: 772.421 secs

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BX381961 BX381961
AL574009 AL574009
AL054280 Drosophil
BX421125 BX421125
BQ144422 NF085H11D
BX356664 BX356664
                                                                                                 BX415926 BX464554
AL538546 AL538546
BX349688 BX349688
BX349688 BX349688
BX335523 BX335523
AL550172 AL550172
AL106004 Drosophil
B195665 HVSMBn000
AL09882 Drosophil
AL01298 Tetraodon
AL060161 Drosophil
AL525224 AL525224
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration of this Backeley Drosophila Genome Project (BDGP). The BGGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitlly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                             AL066051 Drosophil
BX407485 BX407485
                                   BX425797 BX425797
BX381961 BX381961
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopteraygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BX3912854
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ALC78875
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BX360624 BX360624
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BX403654 BX403654
                                                           August 21, 2004, 10:14:02 ; Search time 5109.13 Seconds (without alignments) 11572.836 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Lough the Barkeley (B-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jongs laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Bufffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila Drosophi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 CACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTGCCTCCCGTCGCCGAC 304
                                                                                                                                                          /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 TTTTKSSVTTCSTBTMSKTTSTCSYSYTTCSTVTSYCSSBBCSTTSTCCSTTCSTCTCSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 TIGCCCCAGACGIIGCCGCIGCGICCGGGICIGGACCTCGCCTTCGCCAACCAGCCCGGC
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebrydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 61.8; DB 13; Length 1201; llarity 10.0%; Pred. No. 0.00088; Conservative 160; Mismatches 84; Indels 0;
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                                    organism="Homo sapiens"
                                                                     /mol_type="mRNA"
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/clone="CS0DI072YL05"
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CNS0052P/c
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BX360624 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI072YL05 3-PRIME, mRNA sequence.
BX360624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 TACCGGCGGTGGTTTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATAT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial scorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP from the and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 WSAGGGGGGTGSTSSSSSSTSTSSSSVSSGGKSSTBSSGSBSSSGSSSSSTSBBSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TCATCCAACCACCCTTTGCCCCAGACGTTGCCGCTGCGTCCGGGTCTGGAACCTCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 TCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGGGCCCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TGCCTCCCGTCGCCGACCTGCCACAGCCGGGGCTGCGCGCTGACGGCTGTGGCGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmil: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4982.r
Contact : Feng Liang Email : fliangelifetech.com URL :
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO72CF03NP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAKR19D16"
/clone="lib="RRC1.98"
/note="end: TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 148; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Score 62.4; DB 29
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Homo sapiens
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Best Local Similarity
Matches 44; Conserv
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VS 924
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double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                    145 CAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCTTTGCCCCAGACGTTGCCGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                          205 GCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCCGGCCACTTGGCTCCACTTGGCGA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 GATCAGGCCCAGCGCCCCTCCGCTCCCGTCGCCGACCTGCCACAGCCGGGGCTGCG 324
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16J16 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                   85 CGTCGTGGGCGCGCGCGCGCGCGCGCGCGGCGTTTCTGGGGTGACCGGGTTGATTCT
                                                                                                                                                                                          25 ITGIICCICITGIIICIGCCIAIGIIGCCCGCGCCACCGACCGGICAGCCGICIGGCCGC
                                                                                                                                                          Gaps
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                      ;
0
                                                                                                             Length 1103;
                                                                                                           3.0%; Score 59.4; DB 13; Length 28.0%; Pred. No. 0.0033; tive 93; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 CCCCCCCTYYYTCCSCCCMCCCCCCMYYYMMMC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCTGACGCCTGTGCCCCTGCCCATGACACCTCACCC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fly), genomic survey sequence.
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                                                                                                                                                   95; Conservative
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                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 GCSSSSSSSCSSGSSBYSCCCBCCCBGYCGCYSBVCSSBSSTBSSVGGSBSSTSGTGCK 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequencoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH12FP1.
                                                                                                                                                                                                                                                                                                                                 676 TCWTHTNSNTYTMVTYVTTTHHTYTNTCCYYCCCCCYYCSCCBYBCNTSCSYSYSBCS 617
                                                                                                                                                                                                                                                                                                                                                                        GCCGICGIGGGCGCCAGCGGCGGTACCGGCGGTGGTITCTGGGGTGACCGGGTTGATT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCTTTGCCCCAGACGTTGCCG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCGTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCCCGGCCACTTGGCTCCACTTGGC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGATCAGGCCCCAGCGCCCCTCCGCTCCCGTCGCCGACCTGCCACAGCCGGGGCTG 322
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                             Length 844;
                                                                                                                                                                                                       3.0%; Score 60.2; DB 29; Length llarity 19.4%; Pred. No. 0.0018; Conservative 131; Mismatches 114; Indels
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/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACR11P16"
/clone lib="RRC1198"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1103)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="CL0BA007ZH12"
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-PRIME, mRNA sequence.
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                 TCTGGCCGCCGTCGTGGGGGGCGCGGTACCGGCGGTGGTTTCTGGGGTGACCGG 135
                                                                                                                                                                                                                                                                                                                                                     136 GIIGAIICICAGCCCIICGCAAICCCCIAIATICAICCAACCAACCCCITIGCCCCAGAC 195
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
                                                                                                                                            Gaps
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0
                                                                               Length 1000;
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                                                                                                                                            Conservative 120; Mismatches 159;
                                                                                     DB 13;
                                                                                     57.6; DB 1
No. 0.0085;
Library was not normalized."
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/plasmid="pBeloBAC11"
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/organism="Drosophila
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//db xref="taxon:9606"
//clone="CS0DE005YI19"
//clone lib="Homo sapiens PLACENTA"
//clone lib="Homo sapiens PLACENTA"
//note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NorII-oligo(GT) primer. Five prime end enriched, with a NorII-oligo(GT) primer. Five prime end enriched, with a NorII-oligo(GT) primer. Five prime and cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and Cloned into the Not I and
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11 (bases 1 to 1000)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6789.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgirseq=CSOAS005ZD02QP1&cluster=6789.f. Contact :
Feng Library Evrorem.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOAS005ZD02QP1.
                                                                                                                             73
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                                                                                                                          cechsityngcritchensheiteckecsitreveceetrsetraekeetrsevaebeeete
                                                                                                                                                                                                                                              74 CGICIGGCCGCCGICGIGGCGCCGCAGCGGCGGIACCGGCGGTGGTITCIGGGGTGACC
                                                                   Gaps
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         Length 1013;
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      tch 2.9%; Score 58.2; DB 29; Length al Similarity 26.7%; Pred. No. 0.0061; 108; Conservative 114; Mismatches 182; Indels
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231 861 801

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/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 828)
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cgi-bin/cluster.cgi?seq=CLOBB030ZE01FP1&cluster=8556.f. Contact
cgi-bin/cluster.cgi?seq=CLOBB030ZE01FP1&cluster=8556.f. Contact
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB030ZE01FP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8556.f
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                                                                                                      Length 1203;
                                                                                                                                                Indels
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                                                                                                                                            55; Mismatches 138;
                                                                                                        DB 29;
                                                                                                    2.9%; Score 57.2; DB; 38.5%; Pred. No. 0.012;
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    /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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/db_xref="taxon:9606"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                        1096 TITBSTSTSSTSTITIKITITETITESSBSTSTSTSTETBSBSSSSBBSBBSGSSSSBSS 1037
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375 IGATICICGCGGIGCAATICTACGCCGCCAGIATAATTIGICIACTICACCCCTGACAIC 434
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                                                                                                                                                                                                                         856 SSYGSSSBTCTSKCSTBTSGSTBTSTBMSKBSST-SSTSBTSGSSBCGGSCGSTSGSSCS
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterryota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                         Length 1101;
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                                   2.9%; Score 57.4; DB 29;
llarity 16.6%; Pred. No. 0.01;
Conservative 195; Mismatches 165;
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/db_xref="taxon:7227"
/clone="BACN15E10"
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AL574009 1201 bp mRNA linear EST 31-MAY-2003 AL574009 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI053YA04 3-PRIME, mRNA sequence.
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                                                                      CNCNCMAAKCCNNACKANNNKKKMKACNANNNNKCKMMNNKKKKKKKKCMNKNKKKKKMMNK
                                                                                                          64 ACCEGICAGCCGICIGGCCGCCGICGIGGGCGCGCGCGCGGGGCGGGGCGGTGITC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (base 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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 Mismatches 489;
Conservative 270;
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S Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 ENRY cedex - France

Email: seqref@genoscope.ons.fr Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. Contact: Feng Liang Email: fliangelifetech.com (NL:

Intillength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSOD1072CC03NP1.
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BX381961 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI072YF05 3-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                     Gaps
 pCMVSPORT 6 vector
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                                                                              Length
                                                                                                                Indels
                                                                          2.9%; Score 56.6; DB 13;
llarity 30.0%; Pred. No. 0.014;
Conservative 79; Mismatches 140;
   the Not I and EcoRV sites of the Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI072YF05"
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                                                                                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
EMail: seqref@genoscope.cns.fr, www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10873.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDD1051BA02ND1Lccluster=10873.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Email: fliang@lifetech.com URL:
Feng Liang Consocope sequence ID : CSODI053BA02NP1.

Faraday Avenue Genoscope sequence ID : CSODI053BA02NP1.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone="Ist strand cDNA was primed with a NotI-oligo(dT)
primer- Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                            Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12933798.
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       Full-length cDNA libraries and normalization
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/db_xref="taxon:9606"
/clone="CS0D1053YA04"
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melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Goegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BX421125 CODG001YM04 3-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope. Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BM 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3904.f
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone_lib="RPCI-98"
/note="end : TET3"
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1 (bases 1 to 1201)

1 (hases 1 to 1201)

1 (hases 1 to 1201)

Full-length cDNA libraries and normalization Unpublished (2001)
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BE 191 91006 EVRY cedex - France
Benall: sequefefgenoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen Contact: Feng Liang Email: fliang@lifetech.com URL
http://fulliength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO15CA02NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Drought" /note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days-post-watering timepoints."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 COGGGCTGCGGCGCTGACGGCTGTGGCGCCTGCCCATGACACCTCACCCGTCCCGGAC 372
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2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 993 Std Error: 0.00
Plate: 085 row: H column:
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48.7%; Pred. No. 0.1;
tive 0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dev stage="Pooled timepoints"
                                                                                                                                                                                                                                                                                                                          Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF085H11DT"
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_txef="taxon:9606"
/clone="CS000101W04"
/tissue_type="B_CELLS (RAMOS CELL LINE)"
/cell_line="RAWOS CELL LINE"
/clone_lib="Homo CELLS (RAMOS CELL LINE)"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
Contact: May GD
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NF085H11DT1F1095 Drought Medicago truncatula cDNA clone NF085H11DT
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                                                                                                                http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=cSoDG001BG02NP1&cluster=3904.f. Contact
cgi-bin/cluster.cgi?eeq=cSoDG001BG02NP1&cluster=3904.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODG001BG02NP1.
Location/Qualifiers
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11 Similarity 37.2%; Pred. No. 0.079;
132; Conservative 41; Mismatches 182;
                                                                               more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatula (barrel medic)
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BQ144482.1 GI:20281541
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/db Xref="taxon:9606"
/db Xref="taxon:9606"
/clone=XSODIOISYBOJ3"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
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ORF-2 region
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NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.35, G32P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1980 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
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US-08-259-148A-10

US-08-484-054-10

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PCT-US95-13703-1
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iive 0; Mismatches
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Patent No. 5686239
GENERAL INFORMATION:
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STATE: CA
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1141	RESULT 2 US-08-289-148A-4 is Generoe 4, Application US/08259148A j Sequence 4, Application US/08259148A j Patent No. 574140 j Patent No. 574140 j GENERAL INFORMATION: j APPLICANT: Reyes, Gregory R. j APPLICANT: Twu, Jr-Shin j APPLICANT: Twu, Jr-Shin j APPLICANT: Twu, Albert W. j APPLICANT: Krawczynski, Krzysztof Z. j APPLICANT: Krawczynski, Krzysztof Z. j APPLICANT: Yarbough, Patrice D. j TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
ANGOCCCTANGCCTTTTTTCCTCTTTTTTTTCTCCTTTTTTTTCCCCCCC	901 GACTTTGCCTTAGAGCTTGGCAATCTCACCACCTGTAACACCAATACACGTGTG 960

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                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
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                                                E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
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100.0%; Pred. No. 0;
ive 0; Mismatches
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APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,615
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 1980; Conservative
                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                     ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INDIVIDUAL ISOLATE:
VUMBER OF SEQUENCES:
                                                                                                Palo Alto
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US-08-259-148A-4
                                                                                                                                                COUNTRY:
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INDIVIDUAL ISOLATE: ORF 2, MEXICO, FIGURE
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100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 4600-0093.38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPA: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                 PRIOR AND CATE OF THE AND CATE OF THE AND CATE OF THE APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
FRIOR APPLICATION DATA: APPLICATION NUMBER: US 505,888
FILING DATE: 05-APPLIC-1990
PRIOR APPLICATION DATA: US 420,921
FILING APPLICATION NUMBER: US 420,921
FILING APPLICATION DATA: APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
                                                                                                                                                                                                                                                                           FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-ARRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                    US 870,985
                                                                                                                                                                                                                                                                                                                                                                                                                                              38,615
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870
FILING DATE: 20-APRIL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2055 base pairs nucleic acid
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Best Local Similarity 100.
Matches 1980; Conservative
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APPLICANT: Reyes, Gregory R.

APPLICANT: Twu, Jr. Shin

APPLICANT: Twu, Jr. Shin

APPLICANT: Tam, Albert W.

APPLICANT: Tam, Albert W.

APPLICANT: Krawczynski, Krzysztof Z.

APPLICANT: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
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Patent No. 5770689
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421 TCACCCCTGACATCCTCTGGGCACTAATTTAGTCCTGTATGCAGCCCCCTT 480 421 TCACCCCTGACATCCTCTGGGCACTAATTTAGTCCTGTATGCAGCCCCCCTT 480 481 AATCCGCCTGCGCTGCAGGACGGTACTAATTTAGTCCTGTATGCACCCCCCTT 480 481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATCCACTTATGGCCACAGAGGCCTCC 540 481 AATTATGCACAGTACCGGGACGGACGATCTAATCCGTTACCGGCCCCTAGTGCCTCC 540 541 AATTATGCACAGTACCGGGTGCCGGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT 600 601 GCAGTTGGACGGTTGCCGGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT 600 601 GCAGTTGGACGGGTTGCCGGCTACTATCCGTTACCGGCCCTAGTGCCTAAT 600 601 GCAGTTGGACGGTTATCCATTTCTTCTTCTGTTACCGCCCTAAT 600 601 GCAGTTGGACGTATACTTCCATTTCTTCTTCTTCGTCCAACCCCTAAA 600 602 GCAGTTGGACGTATACTATTCTTCTTCTTCTTCTTCAACCTGCGATA 720 61 TCTGTTGACATGCATAATTCATTCCATTACTTCTTCTTCAACACTGGCATA 720 61 TCTGTTGACATGCTATACTTCCATTACTTCCATCTTCATCAACTGCGATA 720 61 TCTGTTGACATGCTCATACTTCCATTACTTCCATCTTCATCAACTGCGCTTC 780 721 GCACTTGAATTGGTCATACTTCCACTACCTCACTCTTCATCATGTTATGCATA 840 721 GCATCTGAATTGGTCATCCCAAGGGAAGCCCTTCACTACTCTCATGTTATGCATA 840 722 GCATCTGAATTGGTCATCCCAAGCGAAGCCCCTCCGGTTCTTCTCTTCATGTTATGCATA 840 723 GTTGAGACATCTGGTGTTGCTGAGGAAGCCCCTCCGGTTCTTCTCTTCTTTATGCATA 840 724 GTTGAGACATCTGGTGTTGCTGAGGAAGCCCCTCCGGTTCTTCTCTTCTTTATGCATA 840 725 GTTGAGACATCTGGTGTTGCTGAGGAAGCCCCTCCGGGTTGCCCTTTATGCATA 840 726 GTTGAGACATCTGGTGTTGCTGAGGAAGCCCCTCCGGGTTGCCCTTTGGCTTATGCTTATGCATA 840 727 GTTGAGACATCTGGTGTTGCTGAGGAAGCCCCTCCGGTTCTTGTCTTTTTTTT	901 GACTTTGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCACAATACACGTGTG 960

661 TCTGTTGACATGCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720 721 GCATCTGAATTGGTCATCCCAAGCGAGGCCTTACCTACCGCAATCAAGGTTGGCGCTCG 780 721 GCATCTGAATTGGTCATCCCAAGCGAGCGCCTTACCGCAATCAAGGTTGGCGCTCG 780 721 GCATCTGAATTGGTCATCCCAAGCGACGCCTTCACTACCGCAATCAAGGTTGGCGCTCG 780	781 GTTGAGACATCTGGTGTGTGGAGGAGGAGCACCTCCGGTCTTGTCATGTTATGCATA 840 	841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG 900	901 GACTITIGCCTIAGAGCTIGAGITICGCAAICTCACCACCTGIAACACCAAIACACGTGIG 960 	961 TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCGAGGGGCCCGACGGGACTGCGGAGCTG 1020	ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTAACCACACAACTGCAGCCTCAGGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA	GGTGAAGTCGGCGCGCGGGATAGTTCTAACATTAACTTTGTGACAACGCTCCTGGGCGGCGCGGGGCGCGCGGGGCTTACTTA	GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTTATTCCCCCCCGGTTGGTT	GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATGGAGAAATGGTGGAGAGGGTGTGGTGAGCAGGGTGTGAGCAGGGAGCCAACCGTGAAGCTCATGGAGGAATGGCCAAGCGTGAAGCTCATACATGGAAGGAGCTCAGCAG		GATTATGACAACCAGGATGAGGATGGGCCCACCCGTCGCCCTGCGCCATCTCGGCCT		1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTCACTTTGGTG 1500  1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG 1500	1501 AATGTTGCGACTGGCGCAGGCCGTAGCCCGATCGCTTGACTGGTCCAAAGTCACCCTC 1560	GACGGGCGCCCTCCCGACTGTTCAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTT 1		1681 AATACTACTGCTAGTCACCAGATTCTGATTGAAATGCTGCCGGCCATCGCGTCTTT 1740
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APPLICATION NUMBER: US 336,672 FILING DATE: 11-APRIL-1989 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 208,997 FILING DATE: 17-UNE-1988 ATTORNEY/AGENT INFORMATION:	NAME: Sholtz, Cha REGISTRATION NUMBE REFERENCE/DOCKET N TELECOMMUNICATION IN	TELEPHONE: (415) 324-0 TELEPAX: (415) 324-09 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTER.STICS:	LENGIH: 2025 Dase par TYEN: nucleic acid STRANDEDNESS: double	), MOLECULE TYPE: CDNA to mRNA ), HYPOTHETICAL: NO ) ORIGINAL SOURCE: ), INDIVIDUAL ISOLATE: ORF 2, MEXICO, FIGURE 7	OS-07-8/8-741A-4 Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AGGCCTCTTTTGCTGTTGTTCCTCTTG1 	Qy         61 CCGACCGGTCAGCCGTCTGGCGCGTCGTGGTGGCGCGCGGCGGTGGT 120           Db         61 CCGACCGGTCAGCCGTCTTGGCCGCCGTCGTGGGCGCGCGGCGGTACCGGCGGTGGT 120	QY 121 TTCTGGGGTGACCGGGTTGATTCTCAGCCATCCCCTATATTCATCCAACAAC 180	QY         181         CCTTTGCCCAGACGTTGCCGCTGCGGGTCTGGACCTCGCCTTCGCCAACCAGC         240           Db         181         CCTTTGCCCAGACGTTGCGGTTCGGGATCTGGAACCTGGACCTCGCCTTCGCAACCAGC         240	241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTCCCGTCGC  241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTCCCCTCCGTCGC	Oy         301 CGACCTGCCACAGCCGGGGCTGCGGCTGACGGCTGTGGCCCATGACACTCA         360           Db         301 CGACTGCCAAAGCCGGGGCTGCGGCGTGACGCTGTGGCCCATGACACCTCA         360	361 CCGTCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT 361 CCGTCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTAAATTTGTTACTAC	421 TOACCCCTGACATCCTCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTT  421 TOACCCCTGACACTACTCTCTGTGCCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCTTT  431 TOACCCTTCTCTCTCTCTCTCTCTCTCTCTAATTTAGTCTTTATATATA	481 AATCCGCCTCTGCCGCTGCAGACGCTACTAATACTCACATTATGGCCACAGAGCCCTCC  481 AATCCGCCTCTGCCGCTGCAGACGCTACTAATACTCACTTATGGCCACAGAGGCCTCC  481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC	Qy         541 AATTATGCACAGTACCGGGTTGCCCGGGTACTATCCGTTACCGGCCCTAGTGCCTAAT 600           Db         541 AATTATGCACAGTACCGGGTTACCGGGCTACTATCCGTTACCGCCCTAGTGCCTAAT	601 GCAGTTGCAGGCTATGCTATTCTTTCTGGCCTCAAACAACCACAACCCCTACA

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ORF-2 region
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APPLICANT: McAtee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Yarbough, Patrice
APPLICANT: Yarbough, Patrice
APPLICANT: Yarbough, Patrice
APPLICANT: Yarbough, Patrice
APPLICANT: Yarbough, Patrice
APPLICANT: Along Yifan
TITLE OF INVENTION: Hepatitis E Virus Antigens and Met
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathleen M. Desjardins, M.D.
STREET: SO5 Penobscot Drive
CITY: Redwood City
STATE: CA
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APPLICATION NUMBER: US/08/477,292
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 36,373
REPERENCE/DOCKET NUMBER: 36,373
RELECOMMUNICATION INFORMATION:
TELEPRAX: (415)369-9500
TELEFAX: (415)369-0709
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                            US-08-477-292-2; Sequence 2, Application US/08477292; Patent No. 6291641; GENERAL INFORMATION:
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STRANDEDNESS: double
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
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100.0%; Score 1980;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 36,672
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2055 base pairs
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REGISTRATION NUMBER: 33,875
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STRANDEDNESS: double
                                                                ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INDIVIDUAL ISOLATE:
US-07-870-985A-4
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1441 CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTGGTG
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Patent No. 6455492

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Paudley, Daniel W.
APPLICANT: Twu, JF-Shin
APPLICANT: Twu, JF-Shin
APPLICANT: Tam, Albert W.
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1381 TTTTCTGTTCTCCAGCCAATGATGTTCCCCCCCCCCCCC	RESULT 7 US-08-299-148A-2 i Sequence 2, Application US/08259148A i Patent No. 5741490 i GENERAL INFORMATION: APPLICANT: Reves, Gregory R. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Yarbough, Patrice D. TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60 CORRESPONDENESS: ADDRESSEBE: Deblinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Ralo Alto STATE: CA COMPUTER READABLE FORM: MEDION TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Defact In Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICANTION NUMBER: US/08/22,335 FILING DATE: 17-JAN-1992
101   CGACCTGCCAAAGCCGGGGCTGAACGCTGTGGCGCTGACCCTCA 360   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   1	901 GACTTTGCCTTAGAGCTTGAGTTTCGCAATCTGACCACTGAACCCAATACACGTGTG 960 901 GACTTTGCCTTAGAGCTTTGAGTTTCGCCAATCCACCTGTAACCAATACACGTGTG 960 901 GACTTTGCCTTAGAGCTTTGCAATCTCACCCGCCGGGGGCCGGGGCTG 1020 901 TCCCGTTACTCCACCTCCTCGTCCTCCTCCCCCCGGGGGCCGGGGCTGGGGGCTG 1020 1021 ACCACAACTGCAGCACTGCTCACTCCGCCCGAGGGCCCGAGGGCTGGGGGTT 1080 1021 ACCACAACTGCAGCCACCACTCCTCCTCCTCCACTTAACGGGTTA 1080 1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 1021 ACCACAACTGCAGCACACGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 1081 GGTGAAGTCGGCCGCGGGATAGCTCATAACTTAACCTTGCTGACCTCCTCGGC 1140 1081 GGTGAAGTCGGCCGCGGGATAGCTCTAACATTAACTTAACCTTGCTGACCTCCTCGGC 1140 1141 GGGTCCCCGACAATTAATTTCGTCGGCGCGCAACTGTTTTAATCCCGCCCG

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                  AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT
                                    GCATCTGAATTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCCGCTCG
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                                                                                                                                                                                                                                         NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEG ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNa to mENA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MEXICO, FIGURE 7
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-UN-1988
ATORNEY AGENT INFORMATION:
NAME: SACILZ, CHAILES K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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Best Local Similarity 100.
Matches 1980; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MEXICO, FIGURE
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz. Chara-
                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 1980; Conservative
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US-08-484-054-2
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                              1666 CGTGCCAAGCTCTCTCTTTTGGGAGGCCGGCACAAAAGCAGGTTATCCTTATAATTAT 1725
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1966 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG 2025
                                                                                                                                                                                             1786 TCAACCTATACCACCAGGCTTGGGGCCGGTCGGTCGCCATTTCTGCGGCCGCGGTTTTG
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  CGTGGCAAGCTCTCTTTTGGGAGGCCGGCACAACAAAGCAGGTTATCCTTATAATTAT
                                                                                   AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT
                                                                                                                                                                 TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGGTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08484054

Patent No. 5770689

GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Pandley, Daniel W.
APPLICANT: Purdy, Mincel A.
APPLICANT: Tan, Albert W.
APPLICANT: Tan, Albert W.
APPLICANT: Tan, Albert W.
APPLICANT: Tan, Albert W.
APPLICANT: Tan, Albert W.
APPLICANT: Tan, Hepatitis B Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPOSING
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
RIOR APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 505,888
FILING RAPLICATION NUMBER: US 505,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APPLI-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
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FILING DATE: 16-JUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 350 Cambi
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94306
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US-08-484-054-2
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1201 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 1260
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APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr.Shin
APPLICANT: Twu, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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; Pred. No. 0;
0; Mismatches
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
CLASSIPICATION ATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PLING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 17-JAN-1990
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APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UUNE-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 420,921 FILING DATE: 13-OCTOBER-1989
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600
TELEPOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 1980; Conservative 0;
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MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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STRANDEDNESS: double
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                                                                         OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4600-0183.22 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                        FILING DATE: 05-ARR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-ARR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-ARR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/316,672
FILING DATE: 11-ARR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/316,672
FILING DATE: 11-ARR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/316,672
FILING DATE: 11-ARR-1989
ATTORNEY AGENT INFORMATION:
    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 324-0880
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MOLECULE TYPE:
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GATAAGGGTGTTGCTATCCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAG 1320
                                                                                                                                                                 GATTATGACAACCAGCATGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCATCTCGGCCT 1380
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Patent No. 6120988
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Fradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tam, Sequences of Enterically Transmitted
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
                                                                                                                                                                                                                                                                                                                                                         CAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGGGTGACTTTGGTG
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CORRESPONDENCE Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: CA
COUNTRY: USA
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US-08-478-507-10
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301 CGACCTGCCACAGCCGGGCGCTGACGGCTGTGGCCCTGCCCATGACACCTCA 360 5417 CGACCTGCCACACGCGGGCGCTGACGGCTGTGGCCCTGCCCATGACACCTCA 5476 5417 CGACCTGCCGGGGGCTGCGATTCTACGCCGCCAGTGACACCTCA 5476 5417 CCCGTCCGGACGTTGATTCTCGCGCGTGCATTCTACGCCGCCAGTATTGTCTACT 420 [	901 GACTTTGCCTTAGAGCTTGGCAATCTCACCACCTGTAACACCAATACACGTGTG 960  6017 GACTTTGCCTTAGAGCTTGGCAATCTCACCACCACTACACACCATTGCGTGTG 6076  961 TCCCGTTACTCCCACACGTCTCACTCCACCACGAGGGCCGACGGGACTGCGGAGGTG 1020  6077 TCCCGTTACTCCCACCACGTCACTCCACCCCGAGGGCCGACGGGACTGCGGAGCTG 1020  1021 ACCACAACTGCAGCACTCACTCACACACTCCACCTTAACCGGACTGCGGAGCTG 1036  1031 ACCACAACTGCAGCACCACGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080  6137 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080  6137 ACCACAACTGCAGCCACCAGGTTCATGAAAATTACTTAACCTGCTCACACCCCCCGGTT 1200  6197 GGTGAAGTCGGCGCGCGGAAATTACTTAACTTAACTTCCTGCACCCCCCGGTT 1200  6197 GGTGAACTCGCCCGCGCAAAATTAATTTCGTCGCTCTGCTTCACCGCCCCGGTT 1200  6197 GGTGAACTCGCCCGCCACAGAATTAATTTCGTCGCTCTGCTTTAATTCCCGCCCCGGTT 1200  6197 GGTCTCAGCCACACAAATTAATTTCGTCGCTCTGCTTAATTACCTCCGCCCCGGTT 1200  6257 GGGCTCCCGACAAATTAATTTCGTCGGCTGGCGGCAACTGTTTTATTCCCGCCCCGGTT 6316  1201 GTCTCAGCCAATGGCCAACCGTGAAGGCTCTAATACATCAGTGCAACACGTTTTAATTCCCGCCCCGGTT 6316  1201 GTCTCAGCCAATGGCCAACCGTGAAGGCTCTAAACATCAGTTTTAATTCCCGCCCCGGTT 6316  1201 GTCTCAGCCAATGGCCAACCGTGAAGCTCTATACATCAGTGGAAATTCCCGCCCG

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                      AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC
                                              AATTATGCACAGTACCGGGTTGCCCGCGCTTACCGTTACCGGCCCCTAGTGCCTAAT
                                                                                                                                     AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCCTAGTGCCTAAT
                                                                                                                                                                                                                             5717 GCAGTIGGAGGCTATGCTATATCCATTICTTTCTGGCCTCAAACAACCACAACCTACA
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APPLICATION NUMBER: US 07/681,078
PILING DATE: 05-APR-1991
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 05-APR-1990
PILOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
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APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
REGISTRATION NUMBER: 42,995
TELEPONDE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEAGH: 7171 Dasa Pairs
TYPE: nucleic acid
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MOLECULE TYPE: I
HYPOTHETICAL: NO
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100.0%; Pred. No. 0;
ive 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7171 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 1980; Conservative
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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MOLECULE TYPE:
HYPOTHETICAL: N
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NUMBER OF INVENTION: No. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: Shociates
STRESPEE: Defilinger & Associates
STRES: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
COUNTY: USA
ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG
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                                                                                                                              CGTGGCAAGCTCTTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/553,427
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/279,823
APPLICATION NUMBER: US 08/279,823
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FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA: 05-APR-1990
FILING DATE: 05-APR-1990
PRIOR APPLICATION APPR: 05-APR-1990
PRIOR APPLICATION DATE: 13-APR-1890
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Parrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of
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APPLICATION NUMBER: US 07/367,486
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Patent No. 6379891
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PRIOR APPLICATION DATA:
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Gaps

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1741   TCBACCTATACCACCAGGCTTGGGGCCGTTCTGCGGCCGCGGCGGCGGGTTTTG   1800   1741   TCBACCTATACCACCAGGCTTGGGGCCGGTCGCCATTTCTGCGGCCGCGGCTTTTG   1800   6857   TCBACCTATACCAGGCTGGTCGGTCCGGTCGGTCGCCCATTTCTGCGGCCGGGTTTTG   6916   6917   GCTCCACGCTCTGCTGGTCGTTTTGATGTTTTGATTATCCGGGGCGGCGCCC   1860   6917   GCTCCACGCTCGGCTCTGCTGGAGGAGATACTTTTGATTATCCGGGGCGGCGCCC   6916   6917   GCTCCACGCTCTCGGCTCTGCTGGAGGAGATACTTTGATTATCCGGGGCGGCGCCCC   6916   6917   GCTCACGCTCTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG   1920   6917   ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG   1920   6917   ACATTTGATGACTTCTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTCCAG   1930   1921   TCAACTGTCGCTGAGCTCCAGGCTTTAAAGTTAAAGTTAAAGTTGCGGGATTGTAG   1980   1931   TCAACTGTCGCTGAGCTCCAGGCCTTAAAGTTAAAGTTAAAGTTGCGGGATTGTAG   1980   1931   TCAACTGTCGCGTGAGCTCCAGGGTTGTAG   1980   1931   TCAACTGTCGCGTGAGCTCCAGGGTTGTAG   1980   1931   TCAACTGTCGCGTGAGCTCCAGGGTTGTAAGTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG   1980   1931   TCAACTGTCGCGTGAGCTCCAGGGTTGTAGTTGTAG   1980   1931   TCAACTGTCGCGTGAGGCTCTTAAAGTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG   1980   1931   TCAACTGTCGCGTGAGGCTCTTAAAGTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG   1980   1931   1031   TCAACTGTCGCGTGAGCTCTTAAAGTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTGTAG   1980   1931   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   1031   103	RESULT 14 US-08-542-634-2  Sequence 2, Application US/08542634  Patent No. 6214870  APPLICANT: Fuerst, Thomas R.  APPLICANT: Wathough, Patrice O.  TILE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31  CORRESPONDENCE: 31  CORRESPONDENCE: ABSOCiates  STREET: 350 Cambridge Ave., Suite 250  STATE: CA	COUNTRY: USA  ZIP: 94306  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  CURRENT APPLICATION DATA:  APPLICATION DATA:  CLASSIFICATION: 435  ATTONEY/AGENT INFORMATION:  MAME: Fabian, Gary R.  REGISTRATION NUMBER: 33,875  TELECOMMUTATION NUMBER: 4600-0293.30  TELECOMMUTATION NUMBER: 4600-0293.30  TELECOMMUTATION NUMBER: 4600-0293.30	itis E Virus (Mexico Strain) region Score 1957.4; DB 3; Length 2058; Pred. No. 0; 0; Mismatches 6; Indels 3; Gaps	<b>н</b>
CTGTTGGAGGTATGCTATATCCATTTCTTGGCCTCAAACAACCACAACCCCTACA 5776   CTGTTGACATGATCCTTGATCTTCTTCTTGTTCAACCTGGCATA 720	GACTTTGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCGTAACACCAATACACGTGTG GACTTTGCCTTAGAGTTTCGCAATCTCACCACCTGTAACACCCAATACACGTGTG GACTTTGCCTTAGAGCTTTCGCAATCTCACCACCTGTAACACCCAATACACGTGTG TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG TCCCGTTACTCCAGGACTGCTCATCACACCTCCACTTTACCGGCACTAATGGGGTA ACCACAACTGCAGCTCCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA GGTGAAGTCGGCCGCGGGGATAGTTCATAACCTTGCTGACCTTTAACGGGTA GGTGAAGTCGGCCGCGGGATAGCTCAAACATTAACTTGCTGACCTCCTCGGC IIIIIIIIIIIIIIIIIIIIIIIIIIIII	### ### ##############################	1	1681 AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT 1740 

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ORF-2 region
                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
FILING DATE:
CLASSIFICATION:
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                         NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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99.5%;
    ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     2058 base pairs
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STRANDEDNESS: double
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Matches 1974;
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	78 TAG 1980	1978	δλ
	11 CAGTCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGGGTAAAACTCGGGGAGTTG 1980	1921	qa
	.8 CAGICAACIGICGGAGGCICCAAGGCTIAAAGIIAAAGGIAGGGAAAAACIIGAAAAAAAAAA	1918	ò
	1 CACACATTIGATGACTICTGCCCTGAATGCCGCGCTTTAGGCCTCCAGGGTTGTGCTTTTC 1920	1861	đ
<del></del>	8 CACACATITGATGACTICTGCCCTGAAIGCCGCGCTTTAGGCCTCCAGGCTTGTGCTTTC 1917	1858	ò
	11 TIGGCICCACGCICCGCCCTGGCTCTGCTGGAGATACTTTTGATTATCCGGGGCGGGC	1801	qa
	B TIGGCICCACGCICCGCCCTGCTCTGCTGGAGAIACITITGAITAITAICCGGGGCGGCG 1857	1798	δλ
	1 ATTTCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTC	1741	qq
	8 ATTICAACCTATACCACCAGGCTTGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGTT 1797	1738	δδ
	1 TATAATACTACTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCC 1740	1681	qq
	8 TATAATACTACTACTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCC 1737	1678	ζ

Search completed: August 21, 2004, 18:11:08 Job time : 167.394 secs

Sequence Sequence

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sequence 47, Appi Sequence 46, Appi Sequence 10, Appi Sequence 48, Appi Sequence 89, Appi Sequence 89, Appi Sequence 90, Appi Sequence 90, Appi Sequence 6, Appi Sequence 6, Appi Sequence 7, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 129, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi Sequence 139, Appi

i US-09-468-147-165
i US-10-319-745-164
US-10-319-745-164
i US-10-239-090A-45
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i US-10-239-090A-46
i US-10-239-090A-46
i US-10-239-090A-41
i US-10-239-090A-11
i US-09-468-147-89
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984 981 984 984 1020 1020 1389 1389 1389

880.6 6673.6 6673.6 660.8 660.8 640.6 640.6 640.6 640.6 640.6 640.6 640.6 640.6 640.6 640.6

Sequence 3 Sequence 2 Sequence 2

US-10-319-745-195 US-09-468-147-24 US-10-319-745-24

ALIGNMENTS

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Sequence 6, Appli
Sequence 6, Appli
Sequence 44, Appl
Sequence 164, App
                                                                                                                      August 21, 2004, 15:15:13; Search time 885.329 Seconds (without alignments) 10985.769 Million cell updates/sec
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Sequence 2, Al
Sequence 4, Al
Sequence 5, A
Sequence 1, Al
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Sequence 10,
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(gnz_6/ptodata1//pubpna/US07 WEW_PUB.seq:*

(gnz_6/ptodata1//pubpna/US06 WEW_PUB.seq:*

(gnz_6/ptodata1//pubpna/US07 WEW_PUB.seq:*

(gnz_6/ptodata1//pubpna/US07 WEW_PUB.seq:*

(gnz_6/ptodata1//pubpna/US08 PUBCCMB.seq:*

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(gnz_6/ptodata1//pubpna/US10A_PUBCCMB.seq:*

(gnz_6/ptodata1//pubpna/US10B_PUBCCMB.seq:*

enCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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; US-10-165-868-2
) US-09-81-410-10
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US-09-769-066-4
3 US-109-769-066-1
5 US-109-769-066-1
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Maximum Match 1008
Listing first 45 summaries
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                                                                              OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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RESULT 1 US-10-165-868-4 ; Sequence 4, Application US/10165868 ; Publication No. US20030143241A1 ; GENERAL INFORMATION: ; APPLICANT: Reyes, Gregory R. ; TWU, Jr-Shin ; TWU, Michael A. ; Krawczynski, Kzzysztof Z. ; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method ; NUMBER OF SEQUENCES: 22	CORRESPONDENCE ADDRESS:  ADDRESSE: Dehlinger & Associates  STREET: 350 Cambridge Avenue, Suite 250  CITY: Palo Alto  STATE: CA  COUNTEX: USA  ZIP: 94306  COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/10/165,868 FILING DATE: 06-Jun-2002 CLASSIFICATION: <ul></ul>
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	APPLICATION NUMBER: US 208,997 FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R.	\$ g	721 GCATCTGAATTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCG 780 
	REGISTRATION NUMBER: 33,875  TELECOMMUNICATION INFORMATION: TELECOMMUNICATION (415) 324-0880	Qy qa	781 GITGAGACATCTGGTGTTGCTGAGGAGGAGCCACCTCCGGTCTTGTCATGTTATGCATA 840
	TELBEAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 2055 base pairs	çy qa	841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG 900
		\$ a	901 GACTITGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACCAATACACGTGTG 960 
	APPOTABLICAL: NO ORIGINAL SORRE: NO SEQUENCE: NOTIVIDUAL ISOLATE: ORF 2, MEXICO, FIGURE 7 SEQUENCE DESCRIPTION: SEQ ID NO: 4:	y d	961 TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCGAGGGGCCGACGGGACTGCGGGACTG 1020 
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0; Mismatches
                                                                          INDIVIDUAL ISOLATE: MEXICO, SEQUENCE DESCRIPTION: SEQ ID NO:
             TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                          100.0%;
STRANDEDNESS: double
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Matches 1980; Conservative
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TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
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APPLICATION DATA:

APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 11-UNDERER: US 367,486
FILING DATE: 11-UNDERER: US 367,486
FILING DATE: 11-UNDERER: US 367,486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
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REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
FAPPLICANT: Reyes, Gregory R. Pradley, Daniel W. Twu, Jr-Shin Purdy, Michael A. Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2100 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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US-10-165-868-2
      1741
                                                                   1801
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TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
No. US20030124510A1-A/No. US20030124510H1-B Hepatitis Viral
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: Composite Mexico strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                          NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite ?
CITY: Palo Alto
CITY: CA
CUMNRY: USA
ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1980;
100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,410
FILING DATE: 07-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                      Sequence 10, Application US/09851410
; Publication No. US20030124510A1
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R
; Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof Z
Tam, Albert
; Fry, Kirk E
                                                                                                                N
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 7171 base pairs
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SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA
HYPOTHETICAL: NO
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Matches 1980;
            US-09-851-410-10
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	Oy 181 CCCTTTGCCCCAGACGTTGCGCTGCGTCCGGGTCTGGACCTCGCCAACCAGCC 240	Qy         241 CGGCCACTTGGCTCCACTTGGCGACATCAGGCCCAGGGCCCCTCCGGTGGC 300           Db         5357 CGGCCACTTGGCTCCACTTGGCGACATCAGGCCCAGCGCCCCTCCGGTGGC 5416	Qy         301         CBACCTGCCACAGCCGGGGCTGCCGACGGCTCTGGCCCTGCCCATGACACTCA         3.60	OY 361 CCCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT 420	Qy         421 TCACCCCTGACATCCTCTGGCACTAATTTAGTCCTGTATGCCCCCCCTT 480           Db         5537 TCACCCCTGACATCTCTGGCCACTGGCACTAGTCTGTATGCACCCCCTT 5596	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	Qy         541 AATTATGCACAGTACCGGGGTTGCCGTACTATCGGTTACCGGCCCCTAGTGCCTAAT 600           Db         5657 AATTATGCACAGTACCGGGTTGCCCGCGCTACTACCGTTACCGCCCTAGTGCCTAAT 5716	601 GCAGTIGGAGGCTAIGCTAIATCCATITCTIGGCCTCAAACAACAACCACAACCCTACA 660	Qy         661         TCTGTTGAACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA         720           Db         5777         TCTGTTGACATGAATTCCATTACTTCCACTGATGAGATTCTTGTTCAACCTGGCATA         5836		Qy 781 GITGAGACATCIGGIGITGCIGAGGAGGAAGCCACCTCCGGTCTIGICATGITAIGCAIA 840	OY 841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACGGTGCCCTTGGCTTACTG 900	OY 901 GACTITGCCITAGAGCTIGAGITICGCAAICTCACCACGTGTAACACCAATACACGTGTG 960	OY         961         TCCCGTTACTCCAGCACTGCTCCTCACTCCGCCCCAGGGGCCGACGGACTGCGGAGCTG         1020           Db         6077         TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGCCGACGAGACTGCGGAGCTG         6136	OY 1021 ACCACAACTGCACCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080	OY 1081 GGTGAAGTCGGCGGGGATAGCTCTAACATTACCTTACCT	ON 1141 GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGGCAACTGTTTATTCCCGCCCG

	0y 1741 TCAACCTAIACCACCAGGGTCGCGGTCGCGGTTTTCTGGGGCGCGGGGTTTTG 1800 Db 6857 TCAACCTAIACCACCAGGTCGCGTCGCGTTTTCTGGGGCGGGGGTTTTG 1800 dy 1801 GCTCCACGTCTGGCTCTGGGGGGGGGGGGGGGGGGGGGG
CRGANISH: Hepatitis E Virus Mexico (M74506)   Us-10-239-090A-49   Usuary Match   Beat Local Similarity   100.04; Pred. Mo. 0; Indels 0; Gaps 0; Matches 1980; Daily Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1980; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches	661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTC  [

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                                      TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES TOWNERS OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Deblinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                   ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CORPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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FILING DATE: -(Unknown).
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: Hepatitis E Virus
ORF-2 region
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
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  McAtee, C. Patrick
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McAter,
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Yarbough, Pace
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 99.5%;
Matches 1974; Conservative
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                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                       Length 1647
                                                                        LENGTH: 1647 base pairs
TYPE: nucleic acid
STRANDEDNESS: Hepatitis E virus (Mexico strain)
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                       DB 9;
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Pred. No. 0;
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                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCES.
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                         r62kDa, FIGURE
           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 4:
TELECOMMUNICATION INFORMATION
                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity 99.5%;
Matches 1638; Conservative
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                                 GTGAATGTTGCGACTGGCGCGCGGTAGCCCGATCGCTTGACTGGTCCAAAGTCACC
                                                    CTCGACGGGGGGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCALCE, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
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STREET: 350 Cambridge Ave., Suite 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
( APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Patent No. US20020107360A1
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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STATE: CA
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US-09-769-066-4
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; SEQ ID NO 5 ; LENGTH: 1990 ; TYPE: DNA ; ORGANISM: hepatitis E virus US-10-381-770-5	Query Match Best Local Similarity 81.1%; Pred. No. 0; Matches 1608; Conservative 0; Mismatches 372; Indels 3; Gaps 1;	OY 1 ATGCGCCTAGGCCTTTTGCTGTTGTTCCTCTTTTTTTGTGTTGCCCGCGCCA 60	Qy         61 CCGACCGGTCAGCCGTCTGGCCGCCGTCGTGGCGGCGACGGCGTACCGGCGGTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTGGCGCGCGCGCGCGGCG	Qy 121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	Qy 181 CCCTTTGCCCAGACGTTGCCGCTCCGGGTCTGGACCTCGCCTTCGCCAACCAGCC 240	9y 241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCACCCTCCGCTGCCTCCCGTCGC 300	9y 301 CGACCTGCCACAGCCGGGGCTGCGGCTGACGCTGTGGCCCATGACACCTCA 360	Qy 361 CCCGTCCCGGACGTTCATTCTCGCGGTGCAATTCTACGCCGCCAGTATATTGTCTACT 420	OY 421 TCACCCTGACATCTTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCCCCCTT 480	Qy 481 AATCCGCCTCTGCCGCTGCAGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	QY 541 AATTATGCACAGTACCGGGGTTGCCCGCGCTATCGGTACCGGTCCCTAGTGCCTAAT 600	Qy 601 GCAGTIGGAGGCTATGCTATATCCATTTCTTGGCCTCAAACAACCACAACAAC 660	QY 661 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA 720	QY 721 GCATCTGAATTGGTCATCCCAAGCGACGCCTTCACTACCGCAATCAAGGTTGGCGGTCG 780	QY 781 GITGAGACAICIGGIGITGCIGAGGAAGCCACCICCGGICTIGICAIGITAIGCAIA 840	QY 841 CATGGCTCTCCAGTTAACTCCTATACCAGTGCCCTTATACGGTGCCCTTACTG 900	Qy 901 GACTITGCCTTAGAGCTTCGCAATCTCACCACCTGTAACACCAATACACGTGTG 960
Db 781 TTACTTAACCTGACACGCTCCTCGGCGGCTCCCCGACAATTACGTCGGCT 840 QY 1171 GGCGGGCAACTGTTTATTCCCGCCGGTTGTCTCAGCCAACCAA	1231		Qy         1351         CCCACCCGTGGCCTGCGCCATCTGGGCCTTTTTTTGTGTTCTCGAGCAAATGATGTTCTT         1410           Db         1021         CCCACCCGTGGCCTGCGCCATCTGGGCCTTTTTCTGTTCTCCGAGCAAATGATGTACTT         1080	QY         1411         TGGCTGTCCCTCACTGCAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG         1470           Db         1081         TGGCTGTCCCTCACTGCAGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCG         1140	QY         1471         GTTTATALCGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGGGGCGTGGCC         1530           Db         1141         GTTTATALCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCAGCCGTAGCC         1200	QY         1531         CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGCCCCTCCCGACTGTTGAGCAA         1590           Db         1201         CGATCGCTTGACTGGTCCAAAGTCACCCTCGACGGCCCCTCCCGACTGTTGAGCAA         1260	Qy         1591. TATTCCAAGACATTCTTTGTGCTCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGC 1650           Db         1261 TATTCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTTGGGAGGCCGGC 1320	TGATT       TGATT		Qy         1771         CCGGTCGCCATTTCTGCGCCGCGGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGGAG 1830           Db         1441         CCGGTCGCCATTTCTGCGGGCTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGAG 1500	QY         1831         GATACTTTTGATTATCCGGGGCGCGCACATTTGATGACTTCTGCCCTGAATGCCGC         1890           Db         1501         GATACTTTTGATTATCCGGGGCGCACACATTTCATGACTTCTGCCCTGAATGCCGC         1560	TTAAA 		RESULT 7 US-10-381-770-5	; Sequence 5, Application US/10381770 ; Publication No. US20040052813A1 ; GENERAL INFORMATION: ; APPLICANT: YANG SHENG TANG COMPANY 1.1-8	; TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS ; TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS ; FILE REFERENCE: IECO10037PCT ; CURRENT APPLICATION NUMBER: 132/10/381, 770	

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                              Sequence 1. Application US/09769066
Sequenct No. US20020107360A1
GENERAL INPORMATION:
GENERAL INPORMATION:
McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: CURNOWN>
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TYPE: nucleic acid
STRANDEDNESS: Hepatitis E Virus (Burma strain)
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FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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Pred. No. 0;
0; Mismatches
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ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
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415) 324-0960
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ULE TYPE: DNA (genomic)
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ilarity 81.0%;
Conservative
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94306
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Best Local Similarity
Matches 1606; Conserv
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RESULT 8
US-09-769-066-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2049;
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                                                                                                                                                                                                                                                                                                                                                                                                                        FIGURE
                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
FORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 bags pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.1%; Score 1368.6;
81.0%; Pred. No. 0;
:ive 0; Mismatches
                                           APPLICATION NUMBER: US/07/870,985A
                                                                                                                                                                                                                                                                                                                                                                                                                        BURMA,
                                                   FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JNN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 420,486
FILING DATE: 11-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                    APPLICATION NUMBER: US 336,672
FILING DATE: 11.APRLIL-1989
PAPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                                                                                                                        2,
NO:
                   CLASSIFICATION: <Unknown> APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: ORF
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 69.1
Best Local Similarity 81.0
Matches 1606; Conservative
                                                                                                                                                                                                                                                                                                            INFORMATION
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         FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UDNS-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
TELEOROWINICATION INFORMATION:
TELECROWINICATION INFORMATION:
TELEPRONE: (415) 324-0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
69.1%; Score 1368.6;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1606; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2094 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                    1678 TATAATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCGGGCCATCGGGTCGCC
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APPLICANT: Revers, Gregory R.

Twu, Jr-Shin

Purdy, Michael A.

Tam, Albert W.

Krawczynski, Krzysztof Z.

TITLE OF INVENCH. Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/870,985A FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
BITTEN DATE: 150 NUMBER: US 367,486
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
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0; Mismatches
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  strain
                                                                                                                                                NAME/KEY: CDS
LOCATION: 5106..5474
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                CDS
5147..7126
STRANDEDNESS: HEV -
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28..5106
          TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
FEATURE:
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\$490 CGATCTGCCCCAGCTGGGGCCGCTTGACCGCTGTATCACCGGCTCCTGACAGCC 5549  361 CCCGTCCCGGACGTGGGGCTGCGCCGTTTCACCGGCTCCTGACAGCC 5549  362 CCCGTCCCGGACGTGATTCTCGCGGTGCAATTCTACCCGGCAGTACATTTGTCTACT 420  5550 CCTGTGCCTGATTGATTCACGCGGTGCAATTTAGTCCTGTAGTCTGTCCCCCTT 480  421 TCACCCTGACATCTTGTCGCCTCTGGCCTAGTTTATGTCCTGTAGCCCCCCTT 480  5610 TCCCGCTCTGCCGCTCCGGGCCTCCGGCCAAATTTATGCCCACAGGCCTC 540  5610 AATTATGCCCTTCTGCGCTCCGGGCACACACTTATTATGCCCACAGGCCTC 5729  5610 AATTATGCCCCTTCAGGATGCCACACACTTATTATGCCCTAAT 600  5730 AATTATGCCCAGTTATTCCATTTCTTTCTGCCTAATCACCCCTAAT 600  5730 GCAGTTGGAGACTATTCCATTTCTTTTTGGCCCCACACACCCCTACGCCCCTAAT 600  5730 GCAGTTGGAGACTATTCTATTTTTTTTTTTTTTTTTTTT		10.18   CTANCACACACCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGG
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1621 CTCCGCGGTAAGCTCTCTTTTGGGAGCCAGGTACTAAAAGCCGGTACCCTTATAAT 1680   1678 TATAATACTACTGCTAGTGACCAGATTCTGATTGAAAAGCCGCGTCGGCTCGGCTCGCTC	RESULT 13 US-10-239-090A-44  i Sequence 44, Application US/10239090A  i Sequence 40. Application US/10239090A  i Publication No. US20040101820A1  i GENERAL INFORMATION:  i APPLICANT: KABUSHIKI KAISHA TOSHIBA  i TITLE OF INVENTION: From Japanese, chip including the same,  i TITLE OF INVENTION: detecting hepatitis E virus using the same,  i TITLE OF INVENTION: detecting hepatitis E virus using the same  i TITLE OF INVENTION: detecting hepatitis E virus using the same  i TITLE OF INVENTION UNMBER: US/10/239,090A  CURRENT PILING DATE: 2003-07-24  REIOR APPLICATION NUMBER: JP2001-191837  i RIOR PILING DATE: 2001-06-25  i MUMBER OF SEQ ID NOS: 57  i ENGRYH: 7256  i ENGRYH: 7256  i CORGANISM: Hepatitis E Virus Japan JKN-Sap(AB074918)  US-10-239-090A-44	Query Match         66.6%;         Score 1319.6;         DB 17;         Length 7256;           Best Local         Similarity         79.5%;         Pred. No. 0;         DB 17;         Length 7256;           Matches 1575;         Conservative         0;         Mismatches 404;         Indels 3;         Gaps 1;           QY         1         ATGCGCCTAGGCCTTTTTGCTTTTTTTTTTTTTTTTTTT

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Best Local Simi
Matches 1570;
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                      GACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTATATCTCGGACAGCGTGACTTTG
                                         GACCAGACTACGTATGGGTCCACCAACCCTATGTATGTCTCCGACACAGTCACGCTC
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Sequence 164, Application US/09468147A

Publication No. US20030049601A1

SERNERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Desai, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, Serseh M.
APPLICANT: Manbahwar, I. K.
TITLE OF INVENTION: HEFATITIS E VIRUS
TITLE OF INVENTION: HEFATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
CURRENT FILING DATE: 1999-12-21
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1999-10-15
EARLIER PRING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: PastSEQ for Windows Version 3.0

SEC ID NO 164

SEC ID NO 164
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-09-468-147-164
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    Length
                                                                            Indels
    DB 10;
                                                                            406;
Score 1315.2;
Pred. No. 0;
3; Mismatches
                                                                            3;
        66.4%;
                                                Similarity 79.2
70; Conservative
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APPLICANT: Desail, Calcon. T.
APPLICANT: Mushahwar, I. K.
ITILE DE INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 623-US.Pl
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT APPLICATION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 06/061,199
EARLIER PILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FASTSEQ for Windows Version 3.0
| LENGTH: 1277
      Abbott Laboratories
                     APPLICANT: Schlauder, George
APPLICANT: Erker, James C.
APPLICANT: Desai, Suresh M.
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Hepatitis E Virus
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Best Local Similarity 79.2
Matches 1570; Conservative
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LOCATION: (36)...(5159)
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Sequence 165, Application US/09468147A Publication No. US20030049601A1 GENERAL INFORMATION:

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1586107 seqs, 282547505 residues Searched:

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1: geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score         Match Length DB         ID           3408         100.0         660         2         AAR38785         Aar38785           3408         100.0         660         2         AAR38785         Aar38785           3408         100.0         660         2         AAR38785         Aar38785           3408         100.0         660         2         AAR891306         Aar38785           3408         100.0         660         2         AAR38785         Aar38782           3408         100.0         660         2         AAR891389         Aar36822           3408         100.0         660         2         AAR862523         Aar3682120           3408         100.0         660         3         AAB24120         Aar362523           3408         100.0         660         2         AAR71210         Aar70323           3401         99.8         660         2         AAR71210         Aar70323           3391         99.5         660         2         AAR71210         Aar70323           3391         99.5         660         2         AAR71210         Aar70323           3391         99.5         660	ŗ		*			SUMMAKIES	
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4         3408         100.0         660         2         AAW35826         Aaw80197         Aaw80199         Aaw80199         Aaw801819         Aaw80182523         Aab801559         Aab801559         Aab801559         Aab801559         Aab801559         Aab801559         Aab801559         Aab801559         Aab801559         Aab801569         Aaw701210         Aa	r	3408	100.0	099	~	AAR96089	Henati
5         3408         100.0         660         2         AAW80197         Aaw80197           6         3408         100.0         660         3         AAB493389         AAB493389           8         3408         100.0         660         3         AAB493389         AAB493389           9         3408         100.0         660         3         AAB492420         AAB62523           9         3408         100.0         660         5         AAA015699         AAA015699           1         3401         99.8         660         2         AAW70323         Aav70459           2         3401         99.5         660         2         AAW70323         Aav701823           3         3391         99.5         660         2         AAW70323         Aav701814           4         3391         99.5         660         2         AAW93386         Aaw33386           6         5         660         5         ABB1670         AAB50606           8         3391         99.5         660         5         AAB1670           9         3382         99.2         660         5         AAB16803         Aav851265	4	3408	100.0	099	0	AAW35826	
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7         3408         100.0         660         3         AABE4120         AABE4223         AABE4120           9         3408         100.0         660         4         AABE2523         AABE42523         AABE42523           1         3408         100.0         660         7         AAD134376         AABE4376           2         3401         99.8         660         2         AAM71210         AAW7210           3         3391         99.7         660         2         AAR70323         AAR7210           4         3391         99.5         660         2         AAR71210         AAW7210           5         3391         99.5         660         2         AAR70323         AAR731814           6         3391         99.5         660         5         AAB81670         AAB3386           7         3391         99.5         660         5         AAB3060         AAB3336           8         3386         99.4         660         5         AAB12290         AAB12290           9         3382         99.2         660         2         AAR81220         AAR81226           3382         99.2         660	ø	3408	100.0	099	~	AAW93389	Human HE
8         3408         100.0         660         4         AABE2523         Aab62523           9         3408         100.0         660         5         AAD15699         Aac15699           1         3408         100.0         660         2         AAW71210         Aav76369           2         3401         99.8         660         2         AAW71210         Aaw71210           3         3391         99.5         660         2         AAR71210         Aav71210           4         3391         99.5         660         2         AAR71210         Aav71210           5         3391         99.5         660         2         AAR71210         Aav71210           6         2         AAR71210         AAR71210         Aav3336           7         3391         99.5         660         2         AAR3386           8         3391         99.5         660         6         AAB5060         Ada5060           8         3386         99.4         660         5         ABB81670         Ada5060           9         3382         99.2         660         2         AAR51265         Aav851265           1	7	3408	100.0	099	٣	AAB24120	
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0         3408         100.0         660         7         ADD24376         Add24376           1         3401         99.8         660         2         AAW76369         AAW776369         AAW776369           3         3401         99.8         660         2         AAK70323         AAW776369         AAW776369           4         3391         99.7         660         2         AAK70323         AAX71210           5         3391         99.5         660         2         AAK801814         AAW33386         AAW33386           6         3391         99.5         660         5         ABB1670         ADW33386         ADW33386         ADW33386           9         5         660         5         ABB1670         ADW33386         ADW33386         ADW33386           9         5         660         5         ABJ04803         ADW35080         ADW35080         ADW35080           9         3382         99.2         660         5         AAR812290         AAR81220         AAR81220           1         3382         99.2         660         2         AAW33395         AAW33398         AAW933398           3         3377	σ	3408	100.0	099	Ŋ	AA015699	
1         3401         99.8         660         2         AAW76369         Aaw76369           2         3401         99.8         660         2         AAR71210         Aaw71310           4         3391         99.7         660         2         AAR70323         Aar70323           4         3391         99.5         660         2         AAR91814         Aar91814           5         3391         99.5         660         2         AAR93386         Aaw93386           7         3391         99.5         660         5         ABB81670         Ada901670           8         3391         99.5         660         6         ADA60060         Ada50600           9         386         99.4         660         5         AB04803         Adb50600           1         3382         99.2         660         2         AAR51286         Aac12280           1         3382         99.2         660         2         AAW1520         Aaw81520           2         3382         99.2         660         2         AAW3338         Aaw81520           3         3382         99.2         660         2         AAW3338 </td <td>10</td> <td>3408</td> <td>100.0</td> <td>099</td> <td>7</td> <td>ADD24376</td> <td></td>	10	3408	100.0	099	7	ADD24376	
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4         3391         99.5         660         2         AARW3386         Aaw3386           5         3391         99.5         660         2         AARW3386         Abab3086           7         3391         99.5         660         6         AbB61670         Abab50670         Ada50060           8         3391         99.5         660         7         AbB7807         Ada50060         Ada50060           9         3386         99.4         660         5         AbJ04803         Ada507807         Ada507807           0         3383         99.3         660         2         AARE1265         Aax51265         Aax51262           2         3382         99.2         660         2         AARW3355         Aaw81526           3         3382         99.2         660         2         AARW3395         Aaw81526           4         3382         99.2         660         2         AARW3395         Aaw83395           5         3377         99.1         660         5         AbJ04811         AbJ04811	13	3399	99.7	099	~	AAR70323	
5         3391         99.5         660         2         AAW33386         Aaw33386           7         3391         99.5         660         6         ADA50060         Ada50060           8         3391         99.5         660         7         ADB97807         Adb5060           9         3386         99.4         660         5         ABJ04803         Abj04803           1         3382         99.2         660         2         AAR512980         Aac12980           2         3382         99.2         660         2         AAW01520         Aaw81520           3         3382         99.2         660         2         AAW01520         Aaw93395           4         3382         99.2         660         2         AAW33398         Aaw93395           5         3377         99.1         660         5         ABJ04811         Abj04811	14	3391	99.5	099	N	AAR91814	
6 3391 99.5 660 5 ABB01670 Abb81670 8 3391 99.5 660 6 Abb850060 9 3386 99.4 660 7 Abb9803 Abj04803 0 3382 99.2 660 2 AAR812890 Aars12280 2 3382 99.2 660 2 AAR81255 Aars1265 3 3382 99.2 660 2 AAR8155 3 3382 99.2 660 2 AAR8155 5 5 60 2 AAR83388 Aaws3388 5 3377 99.1 660 5 ABJ04811 Abj04811	15	3391	99.5	099	7	AAW93386	
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0 3383 99.3 660 4 AAE12980 Aae12980 1 3382 99.2 660 2 AANE1265 Aar51265 3 3382 99.2 660 2 AAN93150 Aaw81220 4 3382 99.2 660 2 AAN93395 Aaw93395 4 3382 99.2 660 2 AAN93388 Aaw93389 5 3377 99.1 660 5 ABJO4811 Abj04811		3386	99.4	099	2	ABJ04803	
1         3382         99.2         660         2         AANB1265         Aaw81520         Aaw81520           2         3382         99.2         660         2         AAW93395         Aaw93395           4         3382         99.2         660         2         AAW93395         Aaw93395           5         3377         99.1         660         2         AAW93388         Aaw93388           5         3377         99.1         660         5         ABJO4811         AbJ04811		3383	99.3	099	4	AAE12980	
2 3382 99.2 660 2 AAWB1520 AawB1520 Hepati 3 3382 99.2 660 2 AAW93395 Aaw93395 Human 4 3382 99.2 660 2 AAW93388 Aaw93388 Human 5 3377 99.1 660 5 ABJ04811 Abj04811 Abj04811 Hepati		3382	99.2	099	~	AAR51265	
3 3382 99.2 660 2 AAM93395 Aaw93395 Aaw93395 Human 4 3382 99.2 660 2 AAM93388 Aaw93388 Human 5 3377 99.1 660 5 ABJ04811 Abj04811 Hepati		3382	99.2	099	N	AAW81520	
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		37	99.1	099	Ŋ	ABJ04811	12

Aaw93390 Human HEV	Aaw93394 Human HEV	_		Abj04819 Hepatitis							AbiO4001 tropostitis		bhild813 Henstitis		Abi04810 Heratitis			Honor	
AAW93390	AAW93394	AAW93391	ABJ04822	ABJ04819	ABJ04807	AAW93392	ABJ04820	AAR14619	ABJ04806	ABJ04809	AB,104821	AB.104805	AB,104813	ABJ04816	ABJ04810	ABI04818	AAWG33G3	AB, 104804	AAR96090
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0.66	98.9	98.9	98.9	98.9	98.9	98.8	98.7	98.6	98.6	98.6	98.4	98.4	98.3	98.3	98.3	98.3	97.9	96.5	94.5
3374	3372	3372	3370	3370	3369	3367	3363	3361	3360	3360	3353	3352	3351	3351	3350	3349	3336	3290	3221
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

AAR	AAR38785	
Π	AAR38785 stan	AAR38785 standard; protein; 660 AA.
X		
AC	AAR38785;	
×		
Εď	24-OCT-2003	(revised)
Ιď	25-MAR-2003	(revised)
ΤΩ	11-JAN-1994	(first entry)
X		
DE	HEV ORF2 protein.	ein.
X	•	
₹.	Enterically t	Enterically transmitted non-A non-B hepatitis; ET-NANB; vaccine.
ž		
s x	Hepatitis E	Hepatitis E virus; Burma strain.
ЕH	Key	Location/Oualifiers
FT	Peptide	225660
FT		/label= C2
FΤ	Peptide	334660
FI		/label= SG3
FT	Peptide	613660
FI		/label= 406.3-2

93WO-US000459. 92US-00822335. 92US-00876941. WO9314116-A1. 17-JAN-1992; 01-MAY-1992; 15-JAN-1993; 22-JUL-1993. 

(GENE-) GENELABS TECHNOLOGIES INC. (USSH ) US SEC DEPT HEALTH.

Carl Tam AW, Reyes GR, Bradley DW, WPI; 1993-243144/30. N-PSDB; AAQ47129.

Σ

New immunogenic hepatitis E virus (HEV) peptide(s) - are from the ORF1, ORF2 and ORF3 regions of HEV, useful as a vaccine against HEV infection.

Disclosure; Fig 8; 48pp; English.

Immunogenic hepatitis E virus (HEV) peptides are selected from the ORF1, ORF2 and ORF3 regions of HEV. The peptides can be used in vaccines to

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WPI; 1993-243223/30.
N-PSDB; AAQ46813.
                                                                                                   Bradley
                                                                                                                                                                                                                                            Sequence 660 AA;
                                     19-JAN-1993;
                                                             20-APR-1992;
        WO9314208-A2
                       22-JUL-1993
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prevent infection by HEV. The antibodies can neutralise and block HEV infection and can be used to prevent or treat HEV infection. The peptides and antibodies can also be used as diagnostic reagents. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
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                                                                       Score 3408; DB 2;
Pred. No. 5.3e-263;
0; Mismatches 0;
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Best Local Similarity
Matches 660; Conserv
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                                                         Sequence 660 AA;
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14-FEB-1994
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LRGKLSFWBAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600
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C-terminal or
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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1 protein C
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derived from capsid
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                                     92US-00822335.
93WO-US000475
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Matches 660; Conservative
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3 virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
HEV.
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89US-00367486.
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90US-00505888.
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N-PSDB; AAT96959.
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                                                                                                                                                                                                                                                                                                                                       HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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                                                            A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab. where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents the protein from the open reading frame, ORF2, from HEV Burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-field)
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       Diagnosis of hepatitis E virus Burma and Mexico strain infection immunoassay with hepatitis E virus peptide antigens.
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus proteins - useful for diagnosis or vaccine production
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                                                                                  non B hepatitis virus; ET-NANB;
HEV isolate; vaccine; diagnostic probe.
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                                                       Protein encoded by ORF2 of ET-NANB (HEV) Burma strain DNA sequence
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100.0%; Pred. No. 5.3e-263;
iive 0; Mismatches 0;
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                                                                                      non A
Burma
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89US-00336672.
89US-00367486.
89US-00420921.
90US-00505888.
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                                    (first entry)
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non-B hepatitis virus.
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13-OCT-1989;
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25-JUL-1994;
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mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both
                        DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360
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 DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
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experimentally and clinically without fear of
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New DNA sequences of enterically transmitted non-A/non-B (ET-NANB) hepatitis viral agent, useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production.
                                                                             DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
                           DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
                                                            VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ
                                                                                                                      ODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enterically transmitted nonA/nonB viral hepatitis agent; viral;
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100.0%; Pred. No. 5.3e-263;
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                                                                                                                                                                                       TECHNOLOGIES INC.
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89US-00336672.
89US-00367486.
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Best Local Similarity 100.
Matches 660; Conservative
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                                                                                                                                       05-APR-1991;
25-JUL-1994;
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13-OCT-1989;
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11-APR-1989
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are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The present sequence represents a ORF2 protein encoded by a ET-NANB viral
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                                                        Query Match 100.0%; Score 3408; DB 4; Best Local Similarity 100.0%; Pred. No. 5.3e-263; Matches 660; Conservative 0; Mismatches 0;
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                         DNA sequence from HEV-Burma strain
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s strain; bile; ORF2.
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The invention comprises a method for detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a sample and isolating HEV agents or nucleic acid fragments produced by the agent. The method utilises PCR - using bile from a human or cynomolgus monkey actively infected with HEV as a source of the agent. The method of the invention is used for detecting the presence of a viral agent in a sample of cultured cells infected with the agent and isolating enterically transmitted nonA/nonB HEV agents or nucleic acid fragments produced by the agent. The present amino acid sequence represents the protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated from a Burmese strain of the Hepatitis E virus
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100.0%; Pred. No. 5.3e-263;
ive 0; Mismatches 0;
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                                                           88US-00208997.
89US-00336672.
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Matches 660; Conservative
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0; Mismatches 0;
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Matches 660; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a protein derived from an enterically transmitted non-A/non-B viral hepatitis agent. The viral proteins are useful for detecting infection by the enterically transmitted non-A/non-B (ET-NANB/HEV) hepatitis viral agent. The proteins are also useful for producing vaccines for immunising an individual against HEV hepatitis viral agent. The DNA fragments are useful for identifying and sequencing the entire viral agent and for assaying the viral agent in an infected sample. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis
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                                                    DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLST10QYSKTFFVLP
                                                                     DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDMTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                        LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                       LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLOGCAFOSTVAELORLKMKVGKTREL
    QDKGIA1PHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                    QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                                                                                                                                                          LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
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                                                                                                                                                                                                                                                                                                                                                      non-A/non-B viral hepatitis; ET-NANB; HEV; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 8; 81pp; English
                                                                                                                                                                                                                                                                                                                            virus strain Burma ORF 2.
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                                                                                                                                                                                                                                                standard; protein; 660
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89US-00336672.
89US-00367486.
89US-00420921.
9UUS-00505888.
91US-00681078.
94US-00279823.
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                                                                                                                                                                                                                                                                                                  (first entry)
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16-JUN-1989;
13-OCT-1989;
05-APR-1990;
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25-JUL-1994;
03-AUG-1998;
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transmitted nonA/nonB hepatitis virus; identification; HEV;
                                                             Protein encoded by ORF 2 of the Burmese isolate of ET-NANB
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                                                                                                                                                                                                                                                                                                                                      (GENE-) GENELABS TECHNOLOGIES
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89US-00336672.
89US-00367486.
89US-00420921.
                                                                                             ET-NANB; detection; vaccine
                                        (first entry)
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                             (revised)
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                                                                                                                                                     Misc-difference
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13-OCT-1989;
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                                                     Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                        This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in Samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than
                                                                                                                                                                                                                                                                                                                     PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                                                                                                                                                               Length 660;
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                                                                                                                                                                                                                             Score 3401; DB 2;
Pred. No. 1.9e-262;
                                                                                                                                                                                                                                                     0; Mismatches
  EISEI KENKYUSHO.
                                                                                                    Claim 13; Page 24-26; 29pp; Japanese
                                                                                                                                                                                                                             99.8%;
                                                                                                                                                                                                                                      Local Similarity 99.8
les 659; Conservative
KOKURITSU YOBO
                      WPI; 1998-535037/46
                                                                                                                                                                                 previously possible
                                  N-PSDB; AAV61688
                                                                                                                                                                                                         Sequence 660 AA;
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- useful for e.g. virus detection and viral protein

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Yarbough

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Fry

Tam A,

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Krawczynski

90US-00505888 91US-00681078

/note= "not specified"

94US-00279823

Location/Qualifiers

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AAW71209-11 represent the proteins encoded by the open reading frames (ORFs) of the DNA sequence of the Burmese isolate of an enterically transmitted nonA/nonB viral hepatitis agent (ET-NANB). The nucleic acid sequence may be used for identifying and sequencing the entire viral agent (also referred to as HEV), detecting ET-NANB in infected samples, e.g. by specific amplification of virus-derived DNA sequences and for producing recombinant viral proteins for use in vaccines. (Updated on 25 MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                  99.8%; Score 3401; DB 2;
99.8%; Pred. No. 1.9e-262;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                   Sequence 660 AA;
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AAW71210 standard; protein; 660 AA

RESULT 12 AAW71210 ID AAW7 XX Length 660;

DB

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RNA from an HEV strain isolated in the Xinjiang region of China was subjected to RT-PCR to obtain fragments corresp. to ORF2 (given in AAQ86592) and ORF3 (AAQ86593) that encoded antigenic proteins (AAR70123-24, respectively). DNA fragments were manipulated into pGEX vectors for production of GST fusion proteins in E. coli. Applications include HEV infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-2003 to correct PN field.)
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                                        VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ
                                                                                                                              QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                                                                                                                                                               DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                                                                                           LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
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                                                                                                                 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                        DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigens of hepatitis E virus (HEV) - selectively immuno:reactive convalescent and/or acute phase circulating antibodies to HEV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             HEV; ORF2; antigen; vaccine; immunogen
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93AU-00002964
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(first entry)
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28-SEP-1995
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antibody; vaccine; immunisation;
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                                     MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGFWGDRVDSQPFAIPTN
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          2.8e-262;
Score 3399; DE Pred. No. 2.8e-1; Mismatches
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antigen; detection;
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Best Local Similarity 99.7
Matches 658; Conservative
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The present sequence is the protein prod. of ORF-2 from the hepatitis E Virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistan. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. 1gG or 1gM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural luid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysaces of insect cells infected with a HEV ORF-2 contg. boculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781 Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection. DEPT HEALTH & HUMAN SERVICES. 6; Page 13-15; 121pp; English. Local Similarity ... Emerson SU, 1996-209320/21 WPI; 1996-209320/ N-PSDB; AAT27394 Sequence 660 AA; SO (HSSO) Isarev SA, 121 Query Match 61 121 181 241 241 61 181 361 301 301 361 Claim Matches ð qq à g d ò ઠ g ò g δ g ò d

120 120 180 180 240 240 300 300 360 360 420 420 480 540 540 009 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600 480 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL 660 9 9 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAAASRRRPTTAGAAPLTAVAPAHDTP ASELVI PSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLL PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS NYAQYRVARATIRYRPLVDNAVGGYAISISFWPQTTTTFTSVDMNSITSTDVRILVQPGI ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL VGBIGRGIALTLENLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 1 MRPRPILLLLLMFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN DFALELEFRNI TPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP LRGKLSFWEAGTIKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV Gaps ·, 99.5%; Score 3391; DB 2; Length 660; 99.4%; Pred. No. 1.2e-261; Indels 3; 1; Mismatches 541 421 481 481 541 601 421

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Æ 9 AAW93386 standard; protein; (first 11-JUN-1999 AAW93386; RESULT 15 AAW93386

Human HEV ORF 2 protein from strain

Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy; vaccine; immunise; infection; detection; diagnosis; prevention. hepatitis E virus; HEV;

Hepatitis E virus.

WO9904029-A2

17-JUL-1998; 28-JAN-1999

98WO-US014665.

97US-0053069P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Purcell RH; Emerson SU, WPI; 1999-132270/11. × Meng

New isolated swine hepatitis E virus - used to develop products for th diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans.

Example 1; Fig 3A; 70pp; English.

mutants which are capable of cross reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of calls or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or This invention describes a swine hepatitis E virus (HEV) and its natural contamination 

Sequence 660 AA;

ö PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120 9 1 MRPRPILLLLLMFLPWLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFALPYIHPTN Gaps .. 0 Length 660; 3; Indels 99.5%; Score 3391; DB 2; 99.4%; Pred. No. 1.2e-261; 1; Mismatches al Similarity 99.4 656; Conservative Query Match Best Local S: Matches 656 61

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PVPDVDSRGAIIRRQYNLSTSPLISSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180

121

181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI 240

240	300	300	360	360	420	420	480	480	540	540	009	900	660	099
	241 ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGL	241 ASELVIPSERLHYRNOGWRSVETSGVAEEEATSGLVMLCIHGSPVNSYTNTPYTGALGLL	301 DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATREWKDLYFTSTNG	301 DFALELEFRNIIPGNINIRVSRYSSTARHRIRRGADGTAELTITAATRFMKDLYFTSTNG	361 VGEIGRGIALTLFNLADTLLGGLFTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ	361 VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ	421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSFAPSRPFSVLRANDVLWISLTAAEY	421 ODKGIAIPHDIDLGESRVVIODYDNQHEODRPTPSPAPSRPFSVLRANDVLWLSLTAAEY	481 DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQXSKTFFVLP	481 DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP	541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVALSTYTTSLGAGFVSISAVAV	541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV	601 LAPHSALALLEDTLDYPARAHTFDDFCPEGRPLGLQGGAFQSTVAELQRLKOKKVGKTREL	601 LAPHSVLALLEDIMDYPARAHTFDPFCFECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
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Search completed: August 16, 2004, 13:33:47 Job time : 59 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

using sw model - protein search, OM protein

August 16, 2004, 13:28:02 ; Search time 20 Seconds Run on:

(without alignments)
3174.320 Million cell updates/sec

US-09-851-410A-8 3408 Title: Perfect score:

1 MRPRPILLLLLMFLPMLPAP......OSTVAELQRLKMKVGKTREL Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

3408 Result No.

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## ALIGNMENTS

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RESULT 1
VHWWH2
structural protein 2 precursor - hepatitis E virus (strain Burma)
C; Species: hepatitis E virus
C; Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
C; Accession: C40778
R; Tam, A.W.; Smith, M.W.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G. Vicology 185, 120-131, 1991
A; Ttle: Hepatitis E virus (HEV): molecular cloning and sequencing of the full-length vi A; Reference number: A40778; MUID:92024067; PMID:1926770
A; Reference number: A40778; MUID:9330023; PIDN:AAA45736.1; PID:g330026
A; Residues: 1-660 < TAM>
A; Residues: 1-660 < TAM>
A; Residues: 1-660 < TAM>
C; Superfamily: hepatitis E virus structural protein 2
C; Superfamily: hepatitis E virus structural protein
F; 1-22/Domain: signal sequence #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Product: structural protein 2 #status predicted <SIG>F: 23-660/Producted SIG>F: 24-660/Producted SIG>F: 24-660/Prod

Gaps . 0 Indels 100.0%; Score 3408; DB 1; 100.0%; Pred. No. 8.2e-208; ive 0; Mismatches 0;

·.

9 9 IFLPMLPAPPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIHPTN GPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP

120 120 GPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP

180 180 RROYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS RRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS

240 RYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI RYRPLVPNAVGGYAISISFWPQTTTTPTSVDWNSITSTDVRILVQPGI

240

YRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 300 YRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL 300

PGNINTRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDLYFTSTNG 360

FNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ 420

Db 480 DQSTYGSSTGPVYISDSVTLNWATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFULP 539  Qy 541 LRGKLSFWEAGTTKAGYPYNYTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600	unit 3  1862  Mabble membr  Matches: 27-Oct  Cacesion: Sacasion: S  Maftahi, M.;  Mile: Seque  Reference nu  Recession: S  Partie: 11, 567-  Matches: 1-  Tross-refere  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental  Antental	Qy 218 TPTSVDMASITSTDVRILVQPGIASELVIPSERLHYRNQGMSGVETSGVAEEATSGLVM 2/7
QY         421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480           DD         421 QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480           QY         481 DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           DD         481 DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           DD         541 LRGKLSFWBACTTRAQYPNVTTARAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540           QY         541 LRGKLSFWBACTTRAQYPNVTTARSDQLLVBNAAGHRVAISTYTTSLGAGPVSISAVAV 600           DD         541 LRGKLSFWBAGTTRAGYPVNVTTASDQLLVBNAAGHRVAISTYTTSLGAGPVSISAVAV 600	660 660 W.; Tam, A.W. s E virus (HE 60 60 120 120 120 120 240 300	Oy 301 DFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTAATRFMKDLYFTSTNG 360  Db 301 DFALELEFRNLTTCNTNTRVSRYSSTARHS - ARGADGTAELTTAATRFMKDLHFTGLNG 359  Qy 361 VGELEFRNLTTCNTNTRVSRYSSTARHS - ARGADGTAELTTAATRFMKDLHFTGLNG 359  Qy 361 VGELGRGTALTLFNLADTLLGGLPTELISSAGGQLFYSRPVYSANGEPTVKLYTSVENAQ 420  Db 360 VGEVGRGTALTLFNLADTLLGGLPTELISSAGGQLFYSRPVYSANGEPTVKLYTSVENAQ 419  Qy 421 ODKGIAIPHDIDLGESRYVIODYDNOHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480  Db 420 QDKGVAIPHDIDLGBSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 479  QY 481 DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540

ДD		ΩÞ	2777
λ Dp	408 PTVKLYTSVENAQODKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRA 467	Oy Dp	440 IQDYDNQHRQDRPTPSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTG 490 2810 ITASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQ 2865
\$ g	468 NDVLWLSLTAAEYDQSTYGSSTGPVYVSDSVTLVNVATGAQAVAR 512	oy Oy	491 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSF-547 2866 PAGTAITVTL-NGQNYSATTDASGNWS-VTVPASAVSALGEATYSVTASVTNAQGNSSTA 2923
\$ <b>9</b>	513 SLDWTKVTLDGRPLSTIQ	රු සි	548WEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAG 591 2924 SHNVQVNTALPGITINPVATDDIINASEAGSAQTISGQVTGAAAG 2968
oy D	545 LSFWEAGTIKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLG 589 : :	RESULT F90696	5
oy Gb	590 AGPVSISAVAVLAPHSALALLEDTLDYPARA-HT 622 	hypothe C,Speci C,Date: C,Acces	hypothetical protein ECs0542 [imported] - Bscherichia coli (strain O157:H7, substrain RI C;Species: Bscherichia coli C;bate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F90696
RESULT 4 B85547 probable	ו RTX family exoprotein [imported] - Racherichia רחון (פרימות חוקת: אות פייאנות	R,Hayas gasawar DNA Res A,Title	hi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. a, N.; Yssunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. B, 11-22, 2001
C;Specie C;Date: C;Access R:Perna.	Sep-2001	A, Acces A, Statu A, Molec	ence number: Asses; mullilanessi; FMID:11258/96 si preliminary ule type: DNA
iller, I Nature 4 A;Title: A;Refere	iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, L.; Apodaca, Nature 409, 529-533, 2001 A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551	A; kesid A; Cross A; Exper C; Genet A; Genet	A;KeBidues: 1-52/1 (HAY> A;Cros-references: GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: EC80542
A;Status A;Molecu A;Residu A;Cross-	in the type: DNA le type: DNA les: 15:188 < STO> references: GB.AE005174; NID:q12513368; PIDN:AAG54818 1. GSDDR.GN00145. IWGD.704	Query Best Match	Query Match Best Local Similarity 22.3%; Pred. No. 8.2; Matches 131; Conservative 70; Mismatches 235; Indels 151; Gaps 28;
A,Experi C,Geneti A,Gene:		QV DP	60 NPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAA 108 
Query Match Best Local S Matches 131	/ Match 4.1%; Score 139.5; DB 2; Length 5188; Local Similarity 22.3%; Pred. No. 8; Indels 151; Gaps 28; Local 31; Conservative 70; Mismatches 235; Indels 151; Gaps 28;	<i>∂</i> 5 6	109 PLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQD 168 
Qy Dp	60 NPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAA 108 	<i>8</i>	169 GTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPT 220 2578 GGKTYTASVAANGSWSVNVPAADLATLPEGAANVQASVSSASGNSASATHAYSVDASAPT 2637
Qy Dp	109 PLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQD 168       : :	<i>≿</i> 8	221 SVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEFATSGLVMLC1 280 :: :   ::   ::    ::    ::    ::    ::
p da	169 GTNTHIMATEASNYAQYRVARATIRYRPLUPNAVGGYAISISFWPQTTTTPT 220	cy en	281 HGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHR 330
Qy	221 SVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCI 280 ::	y d	331 LRRGADGTAELTTTAATRFMKDLYFTSTNGVGEIGRGIALTLFNLADTLLG 381 2728 LAVDTTAPVLTINTVAGDDIINDAEHAQALVISGTSSGGEAGDVVSVVL 2776
QY	281 HGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHR 330 : :	cy Pp	382 GLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVV 439 2777NGKTYTTTLDASGNWSVGVPAADVTALGSGAQT 2809
Qy Db	331 LRRGADGTAELTTTAATREMKDLYFTSTNGVGEIGRGIALTLFNLADTLLG 381	oy Q	440 IQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTG 490  2810 ITASVSDRAGNSDDASRTVTVSLSAPVISINTIAGDDVINATEKGSDLALSGTSDQ 2865
λŏ	382 GLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIP-HDID-LGESRVV 439	ò	491 PVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSF- 547

: :       : :         :	Db 2386 PFSSPGTATALPALRSTATTPTATSFTALPSSSLGTTW-TRLSQTTTPMATWSTATPSST 2444  Qy 571 VENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLEDTLDYPARAHT 622
RESULT 6 T45025 mucin MUCSB, tracheobronchial [imported] - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45025 R;Desseyn, J.I.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.D.; Laine, A. J; Biol. Chem. 272, 3168-3178, 1997 A;Title: Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alternat A;Reference number: Z22899; MUID:97166151; PMID:9013550 A;Accession: T45025 A;Accession: T45025 A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-3570 cDES> A;Cross-references: EMBL:Z72496; NID:g1834502; PIDN:CAA96577.1; PID:g1834503 A;Gene: MUCSB	RESULT 7 Systam Systam DNA-binding protein R kappa B - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 08-May-1955 #sequence_revision 21-Jul-1995 #text_change 01-Dec-2000 C;Accession: S52863 #45800 R;Nieters A.; Bouwmeester, T.; Scheidereit, C. Submitted to the EMBL Data Library, August 1994 A;Reference number: S52863 A;Steus: preliminary A;Nolecule type: mRNA A;Residues: 1-1324 *NIE> A;Kolecule type: mRNA A;Residues: 1-1324 *NIE> A;Cross references: EMBL:X80878; NID:g695578; PID:g695579 R;Adams, B.S; Leung, K.Y.; Hanley, E.W.; Nabel, G.J. New Biol. 3; 1063-1073, 1991 A;Title: Cloning of R kappa B, a novel DNA-binding protein that recognizes the interleuk A;Reference number: A45580; MUID:92135142; PMID:1777480 A;Accession: A45580
	A;Residues: 313-1292, ISNREQLIAPP',1304,'QSPLLL' <ada> A;Residues: 313-1292, ISNREQLIAPP',1304,'QSPLLL' <ada> A;Cross-references: GB:U08191; GB:S79520; NID:g476273; PIDN:AAA17871.1; PID:g476274 A;Note: sequence extracted from NCBI backbone (NCBIN:79520) C;Keywords: DNA binding; transcription factor</ada></ada>
Db 1867 ALPAINSTATTPTATSVTAIPSSSLGTAWTRLSQTTTPTAI 1907	Query Match 4.0%; Score 135.5; DB 2; Length 1324; Best Local Similarity 19.0%; Pred. No. 2; Matches 131; Conservative 95; Mismatches 232; Indels 231; Gaps 29;
LPLQDG 16    TPG 19	QY 68 AAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTA 105
QY 170 TNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPT 220  DD 1947 TAHTTKVPTTTTGFTATPSSSPGTALTPPWISTTTTPTTRGSTVT 1993	QY 106 GAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLL- 164
QY 221SYDMNSITSTDVRILVQPGIASELJVIPSERLHYRNQGWRSVETSGVAEEEATSGLVML 278	
OY 279 CIHGSLVNSYTNTPYTGALGLLDFALELEF 308	210
QY 309 RNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAAT 347	246
OY 348RPMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAG 392  DD 2157 PHPSSRTTESPPSPGTTTPGHT-RGTSRTTATATPSKTRTSTLLPSSPTSAPITTVVTTG 2215	QY 300LDFALE-LEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAELTTTAATRFM 350 
Qy 393 GQLFYSRPUVSANGEPTVKLYTSVENAQQDKGI 425          : :         : :	QY 351 KDLYFTSTNGVGEIGRGIALTLENLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTV 410
Qy 426AIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAP 458	Qy 411 KLYTSVENAQQDKGTAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRP 461
QY 459 SRPFSVLRANDVLWLSLTAAEYDOSTYGSSTGPVYVSDSVTLVNVATGAQAV 510	462 FSVLKANDVLMLSLTAAEYDQSTYGSSTGPVYVS 1:     :     :     :       :
Qy 511 ARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGTTKAGYPYNYNTASDQLL 570	

	OY 388 ISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPH 429  Db 740 TTGTWTNTGGHLQITGPATLHATTLDNRCGILHTATGPLDLRITGTLNNQDNGLLTTT 797  QY 430 D-IDLGESRVVIQDYDNQH-EQDRPTPSPAPSRPFSVLRANDVLWL
hemagglutinin-like secreted protein XF0889 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 (;Accession: Bg2750 ) C;Accession: Bg2750	Oy 501  Db 913  Oy 561  Db 964
A; Accession: E82750 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-3282 <sim> A; Cross-references: GB: AE003928; GB: AE003849; NID: G9105798; PIDN: AAF83699.1; GSPDB: GN001 A; Experimental source: strain 9a5c A; Eximpson, A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Psimpson, A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Psiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C. A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laign Chado, M.A.; Madeira, M.M.F.; Marino, C.L.; Marques, M.V.; Martins, H.</sim>	MESULT: 9 BESSES  Hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain 9a5c) C;Becies: Xylella fastidiosa C;Bete: 18-Amg-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: B82589 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Status: preliminary A;Molecule type: DNA
Anthors, Grantons, Factorian, M.1.; Menck, C.F.W.; Miracca, B.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, P.J., Santasak A; Authors: da Silva, A.J. de M.; de Silva, A.M.; Silva Jr., W.A.; da Silva; R.A. Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A; Contents: annotation C; Genetics: A; Genetics: A; Genetics: A; Coury Match Best Local Similarity 21.9%; Pred. No. 7.4; Matches 135; Conservative 64: Mismarches 216: Indels 201: Gave 277.	A;Residues: 1-3442 <sim> A;Residues: 1-3442 <sim> A;Residues: 1-3442 <sim> A;CROSs-references: GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF84995.1; GSPDB:GN001 A;Experimental source: strain 945c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docenan, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrichado, M.A.; Madeira, A.M.B.N.; Madeira, A.M.B.N.; Madeira, A.W.; Marrins, E.F.; A;Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menock, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.</sim></sim></sim>
ASRRRPTTAGAAPLTAVAPAHDTPPVPDVDSRGAIL 132	Noutques, V.; KoBa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak. Alauthors: ad Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair. M.; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A; Reference number: A59328 A; Contents: annotation C; Genetics: A; Gene: XF2196
182 182 242 242 589 302 631 336 633 631	Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   Queer   John   John   Queer   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John   John

	Db 631TLTLTGTHTDESHATTTAQQITLHTGDLTTAGGHLTAYGTHTLQLEARTRLD 682  QY 336DGTAELTTAATREMEDLYFTSTNGVGEIGRGIALTLENLADTLLGGLFTEL 387		C;Accession: T21460 B;Witkinson: J. 5. B;Witkinson: J. 5. B;Witkinson: J. 5. B;Witkinson: J. 5. B;Reference number: Z19425 A;Reference number: Z19425 A;Recession: T21460 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil> A;Residues: L-796 <wil-10< th=""><th>QY 63 APDVTAAAGAGPRVRQPARPLGSAWRDQAQRBAVASRRRPTTAGAAPLTAVAPAHDTPPV 122   </th></wil-10<></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil></wil>	QY 63 APDVTAAAGAGPRVRQPARPLGSAWRDQAQRBAVASRRRPTTAGAAPLTAVAPAHDTPPV 122
Db 589 GSLTLTAATL	Oy 430 D-IDLGESRVVIQDYDNQH-EQDRPTPSPAPSRPFSVLRANDVLWL	Db 964 SGTLQIDGTTLTNTGG 979  RESULT 10  B82519  hemagglutinin-like secreted protein XF2775 [imported] - Xylella fastidiosa (strain 9a5c)  c)Species: Xylella fastidiosa  c)Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000  c)Accession: B82519  R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The genome sequence of the plant pathogen Xylella fastidiosa.  A;Reference number: A82515; MUID:20365717; PMID:10910347  A;Recession: B82519  A;Accession: B82519  A;Second Consortium Consortium of the Organization for Nucleotide Sequent Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consortium Consort	A;Cross-references: GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF85560.1; GSPDB:GN001 A;Experimental source: strain 9a5c B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to Genbank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.Contents: annotation A;Contents: annotation A;Gene: XF2775	Query Match 4.0%; Score 135.5; DB 2; Length 3455; Best Local Similarity 21.9%; Pred. No. 8; Matches 135; Conservative 64; Mismatches 216; Indels 201; Gaps 27; Qy 97 ASRRRPTTAGAAPLTAVAPAHDTPPVP

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probable membrane protein YJR151c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J2223; serine/threonine-rich protein YJR151c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S57180
R;Scarcez, T.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57169
A;Reference number: S57169
A;Reference number: S57169
A;Reference number: S57169
A;Reference number: S57169
A;Reference number: S57180
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A;Genes: S6D: NA4; MIPS: YJR151c
A;Cross-references: SGD: S0003912
A;Gene: SGD: DAN4; MIPS: YJR151c
A;Cross-references: SGD: S0003912
A;Map position: 10R
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                                 253 YRNQGWRSVETSGVABEBEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALBLEFRNLT 312
                                                                                                                                                                                                                                                                     368 VSSEAPSTISSSVSSEISSTKSSVMSSEVSSATSSLVSSRAPSAISSL--ASSRLFSSKN 425
                                                                                                                                                                                                                                                                                                                                                                                  426 TSVTSTLVATEASSVTSSLRPSSETLASNSIIESSLSTGYNSTVSTTSAASSTLGSKVS 485
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152 NLVLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRPLVPNAVGGYAISI--
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                                                                                                                SEWPOTITIPISVDMNSITSTDVRILVQPGIASELVIPSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LRGKLSFWEA-GTTKAGYP----YNYNTTASDQLLV-ENAAGHRVAIS 582
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                                                                                                                                                                             88 VITSTVQTTSIEPTTSLVSSNDITTSTSLNISVVISTSTDSTSLIESTTTVGPHASSSVA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9924.09
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23.Feb-1996 #text_change 19-Apr-2002
C;Accession: S59310
R;Churcher, C.M.
Submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Reference number: S59302
                                                SVETSGVAEBEATSGLVMLCIHGSLVNSYTNTPYTGALGLLDFALELEFRNLTPGNTNTR
                                                                                                                                                                                                                                                                                                                                                                                                  240 VDPTSSVVSSAPVDPASSVVSLTSSYPTSSSTVTISANSNGSATLA-----AQTT
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A.Residues: 1-1104 <CHU>
A.Cross-references: BNBL:Z54141; GSPDB:GN00013; MIPS:YMR317w
A.Experimental source: strain AB972
C;Genetics:
A.Gene: MIPS:YMR317w
A.Gene: MIPS:YMR317w
A.Cross-references: SGD:S0004936
A;Map position: 13R
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            PLTAVAPAHDTPPVPDVDSRGAILRR-----QYNLSTSPL-
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213 POTITIPISVDMNSITSTDVRILVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEAT 272
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Virus Genes 7:95-109(1993)
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
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Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
Sequence and gene structure of the hepatitis E virus isolated from
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                                                                                           Indels
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8085BC53CFB46FD3 CRC64;
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Pred. No. 2.7e-207;
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01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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Heparitis B virus (strain Myanmar) (HEV).
Viruses; SSRNA positive-strand viruses, no
Heparitis E-like viruses.
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Matches 656; Conservative
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                                                   NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
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TSATEV S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,

Malik I.A., Igbal M., Purcell R.H.;

"Characterization of a prototype strain of hepatitis E virus.";

Proc. Natl. Acad. Sci. U.S.A. 89:559-563 (1992).

-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING

THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA

BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last amonotation update)
Structural protein 2 precursor (ORP2).
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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  BY BFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA
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70998 MW; 3A82A4EA255C6253 CRC64;
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Pred. No. 8.8e-206;
1; Mismatches 6;
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                                                                                                                                                                                                               InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
Signal.
1 22 BY SIMI
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98.9%;
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est Local Similarity 98.99
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STANDARD;

VST2_HEVME Q03500;

RESULT 4
VST2 HEVME
ID VST2 H
AC Q03500
DT 01-OCT

01-OCT-1993 (Rel. 27, Created)

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                                                                                                                                                                                                                                                                                             "Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                    E virus (HEV).";
Virology 191550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                 J., Yun K.Y., Fry K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 BY SIMILARITY.
659 STRUCTURAL PROTEIN 2.
70640 MW; CF75E75EFDBFBE2C CRC64;
                                                                                               Viruses; ssRNA positive-strand viruses, no DNA Hepatitis E-like viruses.
01-OCT-1993 (Rel. 27, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.0%; Pred. No.
                                                Structural protein 2 precursor.
Hepatitis E virus (strain Mexico) (HEV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M74506; AA445732.1; -.
PIR; B44212; B44212.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                            Huang C.C., Nguyen D., Fernandez J.,
Bradley D.W., Tam A.W., Reyes G.R.;
                                                                                                                                                                                                                          MEDLINE=93079857; PubMed=1448913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Signal.
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23 6
659 AA;
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Matches 614; Conserv
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=31768;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    TKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAVLAPHSALALLED 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G1.";
Mol. Cell. Biol. 16:3264-3274(1996).
PUNCTION: Seems to be involved in the correct timing of cell
separation after cytokinesis, as separation of mutant daughter
cells is delayed. Could either be an enzyme necessary for glucans-
degradation of the cell wall at the neck region between mother and
daughter cells or a requiatory protein controlling this metabolic
step. Exclusively expressed between the end of mitosis and early
G1; inactivated before cells pass start.
              LGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAABYDQSTYGSSTGPV
                                             YVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLPLRGKLSFWEAGT
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EMBL; 246259; CAA86371.1; -.

EMBL; 271603; CAA96259.1; -.

FRBL; 253662; 555862.

PIR; 555862.

GermCohline; 14333; -.

SGD; S0005271; EGT2.

SGD; GO:0009277; C:cell wall (sensu Fungi); IDA.

GO; GO:0009277; C:cell wall (sensu Fungi); IDA.

GO; GO:000910; P:cytokinesis; IMP.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95373280; PubMed-7645347; Maftenin C.; Medlandin C.; Levesque H., Gaillardin C.; Madud U.-M., Levesque H., Gaillardin C.; Medlanding analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PAS8 and KREI loci, five new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovacech B., Nasmyth K., Schuster T.,
"EGT2 gene transcription is induced predominantly by Swi5 in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeas).
Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomycesomy
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGT2 protein precursor (Early G1 transcript EGT2 OR YNL327W OR N0320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1041 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND FUNCTION. MEDLINE=96251274; PubMed=8668141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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SEQUENCE FROM N.A.
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                            480 DQSTYGSSTGPVYISDSVTLVNVATGAQAVARSLDWSKVTLDGRPLPTVEQYSKTFFVLP
                                                                                                                                           DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                            LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                      LAPHSALALLEDTLDYPARAHTFUDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL
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M., Rikihisa T., Mizuno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structural protein 2 (Fragment).

Structural protein 2 (Fragment).
Viruses, ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
NCBI_TaxID=31766;
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Microbiol. Immunol. 36:67-79(1992).
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Pred. No. 1.2e-147;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92261377; PubMed=1584074; Uchida T., Suzuki K., Hayashi N., Iid Wang C.-K., Shikata T., Ichikawa M., Win K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR004261; SP2.
Interpro; IPR008975; Viral_cap_coat.
Pfam; PR03014; SP2; 1.
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NON TER 485 485
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99.0%;
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TZ HEVRH
) VSTZ_HEVRH
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270 PPPPAPATLARPPGHPAGPPTAAPAVPPPAAAQNGGSAGAAPAPAAAGBAG--VSGQP 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 TRVSRYSSTARHRLRRGADGTAELTTTAATRFMKDL----YFTST----NGVGEIGRGIA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------TSSAATETMENVKKCKNFLSTLIKLASSGKQSTETA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPH 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      616 ANVKELVQNLLDG-----KIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTP- 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 IGPVYVSDSVTLVNVATGAQ------AVARSLDWTKVTLDGRPLSTIQQ-YSK 534
                                                                                                                                                                                                                                                                ----PTTAGAAPLTAVAPAHDTPPVPDVDS---RGAILRRQYNLSTSPLTSSVATGTNL 153
                                                                                                                                                                                                                                                                                                                                  154 VLYAAPLSPLLPLQDGTNTHIMATEASNYAQYRVARATIRYRP-----LVP-NAVGGYA 206
                                                                                                                                                                                                                                                                                                                                                                     TLTPTVLAPRLPQPPQNPTNIQ------NFQLPPGMVLVRSENGQLLMIPQQALAQMQ 475
                                                                                                                                                                                                                                                                                                                                                                                                        207 ISISFWPQTTTTPTSVDMNSITSTDVRILVQPG--JASELVIPSERLHYRNQGWRSVETS 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 ATLORSPGVOPOLVLGGAAQTASLGTATAVQTGTP---------QRTVPGATT 579
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                                                                                                                        PMLPAP-----GGGFWGDRVDSQP
                                                                                                                                                                                                                                                                                    370 SMVIGPTMQGALPSPAAVP----PPAPGTPTGLPKGAAGAVTQSLSRTP--TATTSGIRA
                                                                                                                                                                                          FAIPYIHPINPFAPDVTAAAGA-GPRVRQPARPLGSAWRDQAQRPAVASRRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         476 AQAHAQPQTIMAPRPATPTSAPPVQISTVQAPGTPIIARQVTPTIIKQVSQAQTTVQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUSB_HUMAN STANDARD; PRT; 5703 AA.

O9HC84; O00447; O00573; O14985; O15494; O95291; O95451; Q14881; Q95552; Q9HE28;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mucin SB precursor (Mucin 5 subtype B, tracheobronchial) (High molecular weight salivary mucin MG1) (Sublingual gland mucin). MUC5B OR MUC5.
                                                     Length 1083;
                                                                                       Indels
293 293 P -> L (IN REF. 3).
1083 AA; 109943 MW; A6453827572A0752 CRC64;
                                                     DB 1;
                                                                 ilarity 21.1%; Pred. No. 0.5;
Conservative 65; Mismatches 241;
                                                                0.5;
                                                   4.0%; Score 137.5;
21.1%; Pred. No. 0.5
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                                                                   Local Similarity
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                                                                                    Matches 129;
 CONFLICT
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Mol. Cell. Biol. 20:340-351(2000).

-! FUNCTION: Makes part of TFIID is a multimeric protein complex that
-! FUNCTION: Makes part of TFIID is a multimeric protein complex that
-! FUNCTION: Makes part of TFIID is a central role in mediating promoter responses to various
activators and repressors. Potentiates transcriptional activation
by the AF-2S of the retinoic acid, vitamin D3 and thyroid hormone.
-! SUBUNIT: FIID is composed of TATA binding protein (TBP) and a
number of TBP-associated factors (TAF9). Component of the TFTC-HAT
complex, at least composed of TAF5L, TAF6L, TAD31L, SUPT3H/SPT3,
TAF2/TAFII150, TAF4/TAFII135, TAF5/TAFII100, GCNSIZ/GCNS, TAF10
                                                                                                                                                                                                                                                                                 "The human TFIID components TAP(II)135 and TAF(II)20 and the yeast SAGA components ADA1 and TAP(II)68 heterodimerize to form histone-like
                                                                                  Brand M. Yamamoto K., Staub A., Tora L.;
"Identification of TATA-binding protein-free TAFII-containing complex subunits suggests a role in nucleosome acetylation and signal
                                                                                                                                                                                                                                 MEDLINE=20063193; PubMed=10594036;
Gangloff Y.-G., Werten S., Romier C., Carre L., Poch O., Moras D.,
                                      DENTIFICATION IN THE TFTC-HAT COMPLEX WITH TAF5L; TAF6L; TADA3L;
                                                                                                                                                                                              OF 870-918 IN COMPLEX WITH
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G -> GPG (IN REF. 2).
MISSING (IN REF. 3).
   Natl. Acad. Sci. U.S.A. 93:13611-13616(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE TAP2C FAMILY.
                                                      SUPT3H; TAF2; TAF5; TRRAP; GCN5L2 AND TAF10.
MEDLINE=99303588; PubMed=10373431;
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J. Biol. Chem. 274:18285-18289(1999)
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EMBL; AL137077; CAC36006.1; -.
EMBL; AL109911; CAC22312.2; -.
EMBL; V173309; AAC50901.1; -.
PDB; LH30; 26-SEP-02.
TRANSPAC; T02328; -.
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InterPro; IPR006208; Cys knot.
InterPro; IPR006208; Cys knot.
InterPro; IPR006209; Cys knot.
InterPro; IPR009041; PMP_inhibitor.
InterPro; IPR001919; TIL_Cysrich.
InterPro; IPR001055; VVC_out.
InterPro; IPR001065; VWF_C.
InterPro; IPR0010846; VWF_D.
Pfam; PF00007; Cys knot; 1.
Pfam; PF00007; Cys knot; 1.
Pfam; PF00009; VWC; 1.
Pfam; PF0001816; VWC, 6.
SMART; SW00216; VWC, 6.
SMART; SW00216; VWD, 4.
SMART; SW00216; VWD, 4.
PROSITE; PS01128; CTCK 1; 1.
PROSITE; PS01128; CTCK 1; 1.
PROSITE; PS01128; CTCK 2; 1.
PROSITE; PS01128; CTCK 1; 1.
PROSITE; PS01128; CTCK 2; 1.
PROSITE; PS01128; CTCK 2; 2.
Glycoprotein; Repeat; Signal; Polymorphism
      entities requires a license agreement (or send an email to license@isb-sib.ch)
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EMBL; X74955; CAA52910.1; -
EMBL; UG3836; AAB61398.1; -
EMBL; U78554; AACS1344.1; -
EMBL; U78552; AACS1344.1; -
EMBL; U78553; AACS1344.1; JOINED.
EMBL; U78551; AACS1344.1; -
EMBL; U95531; AACS1343.1; -
EMBL; U95531; AACS1343.1; -
EMBL; X09788; CAA70926.1; -
                                                  EMBL; AF107890; AAG33673.1; -. EMBL; AF086604; AAC67545.1; -. EMBL; AJ004862; CAA06167.1; -.
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
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MEDLINE=99023932; PubMed=9804771;

Desseyn J.-L., Buisine M.P., Porchet N., Aubert J.-P., Laine A.;

"Genomic organization of the human mucin gene MUC5B: cDNA and genomic sequences upstream of the large central exon.";

J. Biol. Chem. 273:30157-30164(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen P.A., Bennett E.P., Wandall H.H., Therkildsen M.H., Hannibal J., Clausen H.; Mandall H.H., Therkildsen M.H., "Identification of a major human high molecular weight salivary mucin (MGI) as tracheobronchial mucin MUC5B."; Glycobiology 7:413-419(1997).
                                                                                                                                                                                                                                                                                                                                          "Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alternate subdomains resulting in a super-repeat. Structural evidence for a 11p15.5 gene family."; J. Biol. Chem. 272:3168-3178(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Gall bladder;
MEDLINE=97293229; PubMed=9164870;
Keates A.C., Nunes D.P., Afdhal N.H., Troxler R.F., Offner G.D.;
"Molecular cloning of a major human gall bladder mucin: complete C-ternthal sequence and genomic organization of MUCSB.";
Biochem. J. 324:295-303(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Sublingual gland;
MEDLINE-96125355; PubMed-8554565;
Troxler R.F., Offenr G.D., Zhang F., Iontcheva I., Oppenheim F.G.;
"Molecular cloning of a novel high molecular weight mucin (MG1)
from human sublingual gland.";
Biochem. Biophys. Res. Commun. 217:1112-1119(1995).
[2]
SEQUENCE OF 1-1325 FROM N.A.
MEDLINE=99009274; PubMed=9790959;
Offiner G.D., Numes D.P., Keates A.C., Afdhal N.H., Troxler R.F.;
"The amino-terminal sequence of MUC5B contains conserved
"The amino-terminal sequence of mucin for tissue-specific mucin multifunctional D domains: implications for tissue-specific mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desseyn J.-L., Aubert J.-P., Porchet N., Laine A., Genomic organization of the 3 region of the human MUCSB mucin.", J. Biol. Chem. 272:166373-16883 (1997).
-!- FUNCTION: Salivary mucin that is thought to contribute to the
                                                                                                                                                                                                                                                                           TISSUE=Placenta;
MEDLINE=97166151; PubMed=9013550;
Desseyn J.-L., Guyonnet-Duperat V., Porchet N., Aubert J.-P.,
                                                                                                                Biochem. Biophys. Res. Commun. 251:350-355(1998)
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MEDLINE=97347489; PubMed=9201995;
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TISSUE=Salivary gland;
MEDLINE=97292540; PubMed=9147051;
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28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical serine/threonine-rich protein C19G12.16c in chromosome
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Schizosaccharomyces pombe (Fission yeast).
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                                                   459 SRPFSVLRANDVLWLSLTAAEYD----
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EMBL; AL021813; CAA16975.1; -.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3319 PSSIPGTTHTATVLTTTTTVATGSMATPSS------STQTSGTPPSLTTTATTIT 3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3369 AT-GSTINPSSIPGTIPIPPVLITIAITPAAISSIVIP-SSALGIIHIPPVPNITAITHG 3426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3482 PHPSSRTTESPPSPGTTTPGHT-RGTSRTTATATPSKTRTSTLLPSSPTSAPITTVVTTG 3540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSLPPSSPHTVPTAWTSAT----SGILGTTHITEPSTGTSHTPAATTGTTQPSTPALSS 3481
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Pred. No. 5.1;
72; Mismatches 257; Indels 240;
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G -> E (IN REF. 2).
FPGLCN -> LPCLCK (IN REF. 2).
E -> K (IN REF. 1).
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T -> S (in dbSNP:2672788)
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RK -> GR (IN REF. 2).

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GAA -> AH (IN REF. 3).

A -> S (IN REF. 3).
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
         01-NOV-1995 (Rel. 32, Created)
U-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hansenula MRAXII killer toxin-resistant protein 1 precursor.
                                                                                                       SEQUENCE FROM N.A.
                                                HKR1 OR YDR420W.
                                                                                     NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                   -----GTGSATFTSSPP 347
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tive 77; Mismatches 235; Indels 160;
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                                     PROTEIN C19G12.16C.
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     Hypothetical protein; Glycoprotein; Signal. SIGNAL 1 19
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SPombe; SPAC19G12.16c;
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670 AA;
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1802 AA

PRT;

STANDARD;

HKR1_YEAST ID HKR1_YEAST

RESULT 10

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    J. Bacteriol. 176:1488-1499(1994).
    -!- FUNCTION: Could regulate beta-glucan synthesis. Overexpression provides resistance to Hm-1 killer toxin.
    -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
    -!- PTM: Could be O-glycosylated in the serine/threonine-rich domain.
    -!- SIMILARITY: SOME, TO YEAST MSB2.

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SER/THR-RICH.
SLA 28 AA TANDEM REPEATS OF S-[AV]-[P]-
V-A-V-S-S-T-Y-T-S-S-P-S-A-P-A-R-I-S-S-T-
Y-T-S-S-P
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HANSENULA MRAKII KILLER TOXIN-RESISTANT
MEDLINE=94156857; PubMed=8113191;
Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
Yabe T., Nakajima T., Ichishima E., Furnichi Y.;
"Cloning of the Saccharomyces cerevisiae gene whose overexpression overcomes the effects of HM-1 killer toxin, which inhibits beta-glucan synthesis.";
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19.0%; Pred. No. 1.9;
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61; Mismatches 228; Indels
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InterPro; IPR00211; Cat channel_TrpL.
InterPro; IPR001024; ilpoxygenase_LH2.
InterPro; IPR001024; ilpoxygenase_LH2.
InterPro; IPR000203; PKD_Cys_rich.
InterPro; IPR0008976; PLAT_LH2.
Pfam; PF00125; GPS; 1.
Pfam; PF01477; PLAT; 1.
PF1mTS; PR01437; PLAT; 1.
PR1NTS; PR01437; POLYCYSTIN2.
SWART; SM00308; LH2; 1.
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EMBL; Z48544; CAB70201.1; JOINED. WormPep; ZK945.9; CE25687.
                                                                                                                                EMBL; Z48544; CAB70192.1; -.
EMBL; Z48582; CAB70192.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VTGLSHNFVDSSKSATSFGYSSSSISSIKLSKETIPASKSVSNTQERITSFTSTLRANSQ 1094
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        GAAPLTAVAPAHDTPPVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLP 165
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                                              --FAAISSGYTP
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Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential)
-!- SIMILARITY: Contains 1 GPS domain.
-!- SIMILARITY: Contains 1 PLAT domain.
                                                                                          LQDGTNTHIMATEASNY------AQYRVARATIRYRPLVPNAV--
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Caenorhabditis elegans.
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Wilkinson-Sproat J.;
Submitted (FEB-1995)
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Best Local
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                    ELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQQDKGIAIPHDIDLGESRVVIQDYDN 445
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                                                                                658 TTIESESSTSAVASSTSSTPSTPSSTLSTSTVTEPSSTRSSDSTTTSAGSTTTLQESTTT 717
TFYDSTSVNLTLNSGLGIIGYQTSIECTSPTSSNYVSTTKDGACFTKSVSMPRLGGTYPA
                                        ---VYIQEYSS
                                                            QH-EQDRPT-----PSPAPSRPFSVLRANDVLWLSLTAAEYDQSTYGSSTGPVYVS---
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01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 138.1 kDa protein in FLO9-GDH3 intergenic precursor.
                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                       MEDLINE=55249563; PubMed=7731988;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C
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                                                                                                      -- DSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVL
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InterPro; IPR001389; Flocculin.
Pfam; PF00624; Flocculin; 13.
Hypothetical protein; Glycoprote SIGNAL 1 24 POI
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Hall J., Ouel
Storms R.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSVATGTNLVLYAAPLS-----PLLPLQDGTNTHIMATEASNYAQYRVARATIRYR 195
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01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glucoamylase S2 precursor (BC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
(1,4-alpha-D-glucan glucohydrolase) (GAII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 GESRVVIQDYDNQHEQDRPTPSPA----PSRPFSVLRANDVLWLSLTAAEYDQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGDRVDSQPFAIPYIHPTNPFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                    166;
888 N-LINKED (GLCNAC. . .) (POTENTIAL)
1322 AA; 138072 MW; AADFDIFF13267CEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             92; Mismatches 289;
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                                                                                                                                                                                                                                                    Score 131;
Pred. No. 1
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us-09-851-410a-8.rsp

283

-EYD 481

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                                                                                                                                                                                                                                                                               LVNSYT---NTPYTGALGLLDFALELEFRNLTPGNTNTRVSRYSSTARHRLRRGADGTAE 340
                                                                                                                                                                                                                                                                                                                                                                                 LITTAATREMKDLYFTSTNGVGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRP 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GEYTTEATAPVTTAV-----GTNSAGK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTSYTTKSVPTTY-----VFDFGKG1-----LDQSCGG----VFSNNGSSQVQLRD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VENAQQDKGIAIPHDID-LGESRVVIQDYDNQHEQD 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PSILPGVVIASPSQTHPDYFYQWIRDSALTINSIVSHSADPAIETLLQYLNVSFHLQRT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVLMNG--TV-VYDSNGAWDSSPLEEWLQRQKKVSIERIFENIGPSAVY-----364
TITTTVCSTGINSAGETTSGCSPKIITTTVPCSTSPSETASESITTSPTTPVTVVSTTV
                                                                                                            SFWPOT-TTTPTSVD
                                                                                                                                                                              MNSITSTDVRILLVQPGIASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGS
                                                                                                                                                                                                                           -----TSGCSPKTVTT--TVPCSTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21113168; PubMed=11160904; Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry C.V.; Cohen B.D., Sertil O., Abramova N.E., Davies K.J., Lowry C.V.; "Induction and repression of DAN1 and the family of anaerobic mannoprotein genes in Saccharomyces cerevisiae occurs through complex array of regulatory sites."

Nucleic Acids Res. 29:799-808(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 RPT-----PSPAPSRP-----FSVLRANDVLWLSLTAA-
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-!- SIMILARITY: Belongs to the SRP1 / TIP1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Cell wall protein DAN4 precursor.
                                                                         MATEASNYAQYRVARATIRYRPLVPNAVGGYAISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1161 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVSANGEPTVKLYTS----
                                                                                                                                                                                                                                TNSAGET
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Submitted (SEP-1995)
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P47179;
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or send an email to license@isb-sib.ch).
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INTERACT WITH SUBSTRATES (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the ch
                                                                                                                                                   MEDLINE=91276266; PubMed=2055484;
Lambrechta M.G., Pretorius I.S., Sollitti P., Marmur J.;
"Primary structure and regulation of a glucoamylase-encoding gene
(STA2) in Saccharomyces diastaticus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000165; Glyco hydro_15.
InterPro; IPR008928; Glyco_trans_6hp.
Pfam; PR00723; Glyco hydro.15; 1.
PRINTS; PR00736; GLHYDRLASE15.
PROSTITE; PS00820; GLHOOMYLASE; 1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
Kim K., Bajszar G., Lee S.Y., Knudsen F., Mattoon J.R.; "Cloning of a new allelic variant of a Saccharomyces diastaticus glucoamylase gene and its introduction into industrial yeasts."; Appl. Biochem. Biochem. 14:161-185(1994).
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                                                                                                                                                                                                                                                                                                       glucose residues successively from non-reducing ends of with release of beta-D-glucose.
-!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
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Y SÜBÜNIT.
SÜBSTRATE (BY SIMILARITY)
CATALYTIC BASE (BY SIMILA
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                                                   EMBL; Z4965; CMCC.

PIR; S57180; S57180.

GermOnline; 141984; -.

SGD; S0003912; DAN4.

GO; 0009277; C:cell wall (sensu Fungi); IDA.

InterPro; IPR00092; SRP1 TIP1.

PROSITE; PS00724; SEP1 TIP1.

PROSITE; PS00724; SEP1 TIP1.

Cell wall; Glycoprotein; Membrane; GPI-anchor; Signal; Lipoprotein.

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REMOVED IN MATURE FORM (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 130.5; DB 1; Length 1161;
                                                                                                                                                                                                                                                                                                                                                             GPI-anchor amidated asparagine
                                                                                                                                                                                                                                                                                                                                                                                                              7954C15D69F0CA58 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        (Potential)
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send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                 1161 AA; 118358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%;
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                                                EMBL; Z49651; CAA89684.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 104; Conservative
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1146
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: May modulate neuronal adhesion and neurite growth during development by binding to neural cell adhesion molecules (NG-CAM
                                                                                                                                                                                                                                                           SEQUENCE OF 1-990 AND 1007-1321 FROM N.A., AND VARIANT ALA-1254.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Kromiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of an ~1 Mb region containing the MEF2B gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 2 link domains.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
-!- SIMILARITY: Contains 1 Sushi (SCR) domain.
-!- SIMILARITY: Belongs to the aggrecan/versican proteoglycan family.
10-OCT-2003 (Rel. 42, Last annotation update)
Neurocan core protein precursor (Chondroitín sulfate proteoglycan
CSPG3 OR NCAN OR NEUR.
                                                                          Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                      Prange C.K., Pennacchio L.A., Lieuallen K., Fan W., Lennon G.G., "Characterization of the human neurocan gene, CSPG3.";
Gene 221:199-205(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM, 600826; -...
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR06209; EGF_like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin_C.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                                       MEDLINE=99013874; PubMed=9795216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF026547; AAC80576.1; -.
EMBL; AC003110; AAB86655.1; -.
EMBL; AC005254; AAC25581.1; -.
                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01265; LINKMODULE.
ProDom; PD000918; Link; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin c; 1.
Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P00740; 1EDM.
: HGNC:2465; CSPG3.
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Pfam; PF00047; ig; 1.
                                                            (Human)
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=9606;
                                                            Homo sapiens
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                                                                          PROSITE; PS50U941; C11.3. PROSITE; PS50U941; C11.3. PROSITE; PS60126; EGF 2; 1. PROSITE; PS60126; EGF 2; 1. PROSITE; PS60126; EGF 2; 1. PROSITE; PS60136; EGF CA; 1. PROSITE; PS60137; EGF CA; 1. PROSITE; PS60137; EGF CA; 1. PROSITE; PS60134; LIKK; 2. Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain; PROSITE; PS60131; Calcium; Repeat, Lectin; Sushi; Signal; Polymorphism. SIGNAL 1 22 POTENTIAL. POTENTIAL. 23 1321 POTENTIAL. POTENTIAL.
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22.0%; Pred. No. 2.1;
Live 63; Mismatches 231; Indels 201; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
C-TYPE LECTIN.
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/FIId=VAR 016176.

N -> Y (IN REF. 2).

G -> R (IN REF. 2).

MW, 2EF47F823DB980B8 CRC64;
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   ASX HYDROXYL; 1.
C TYPE LECTIN 1; 1.
C TYPE LECTIN 2; 1.
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Best Local Similarity 22.0°
Matches 140; Conservative
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764 AESPTSGLQATVDEVQDPWPSVYSKGLDASSPSAPLGSPGVFLVPKVTPNLEPWVATDEG 823
                                                                                          824 PTVNPMDSTVTPAPSDASGIWEPGSQVP--EEAESTTLSPQVALDTSIVTPLTTLEQGDK 881
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Search completed: August 16, 2004, 13:34:13 Job time : 17 secs

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August 16, 2004, 13:24:37; Search time 42 Seconds (without alignments) 4958.143 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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6: sp mammal:*
7: sp mhc:*
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9: sp_bhage:*
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Query Match 99.5%; Score 3392; DB 12; Length 660; Best Local Similarity 99.5%; Pred. No. 1.2e-213; Matches 657; Conservative 0; Mismatches 3; Indels 0;

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J. Gen. Virol. 80:1691-1700(1999).
J. Gen. Virol. 80:1691-1700(1999).
EMBL; AF124407; AAA045493.1;
GO; GO:0001918; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
SEQUENCE 660 AA; 71041 MW; 03B72DDF0AB7B521 CRC64;
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MEDLINE=99105430; PubMed=9880424;

TSarev S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Inmis B.L.;

"Phylogenetic analysis of hepatitis E virus isolates from Egypt."

"Phylogenetic analysis of hepatitis E virus isolates from Egypt."

"Med. Virol. 57:68-74[1999).

EMBL; AF051351; AAG35761.1;

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR004261; SP2.

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SEQUENCE FROM N.A.
MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.W., Guerra M.E., Huang C.-C., Bradley Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequenci full-length viral genome.";
Virology 185:120-131(1991).
                       CRC64;
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Pred. No. 5.3e-213;
1; Mismatches 5;
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Hepatitis E virus.
Viruses: sBRNA positive-strand viruses,
Hepatitis E-like viruses.
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MEDLINE=95176571; PubMed=7871758;
Yin S. Purcell R.H., Emerson S.U.;
'An aw Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
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Hepatitis E-like viruses.
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"Identification of the 5' Capped and 3' Complete Terminal Sequence in the Hepatitis E Virus Isolated From Morocco.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065661; AAD10627.1; -.
EMBL; AX230202; AAO72992.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
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MEDLINE=99107414; PubMed=9892396;
MEDLINE=93107414; PubMed=9892396;
Khudyakov Y.E.;
Khudyakov Y.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein 2 (Structural viral protein).
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InterPro; IPR008975; Viral_cap_coat.
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                      MEDINE=92261377; PubMed=1584074;
Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno K., Win K.M.;
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Fry K.E., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
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MEDLINE-93348763; PubMed=8346669;
Bi S-L., Furdy M.-A., McCaustland K.A., Margolis H.S., Bradley D.W.;
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KBMB; L08816; AAA01191.1; ---
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00426; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Malik I.A., Iqbal M., Purcell R.H.;
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Proc. Natl. Acad. Sci. U.S.A. 89:559-563 (1992).
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SEQUENCE FROM N.A.
MEDLINE=92335008; PubMed=1630924;
Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T., Zhuang H.,
Win K.M.;
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B58F23955FDD6614 CRC64;
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Best Local Similarity 99.1'
Matches 654; Conservative
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SEQUENCE FROM N.A.
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      PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                             PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                                                                  181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI
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Uchida T.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; D11033; BAA01867.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete genome sequence.
Hepatitis E virus.
Viruses, seaths positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
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InterPro; IPR008975; Viral_cap_coat.
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SEQUENCE FROM N.A.
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PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                                                                                                                                ASELVIPSERLHYRNQGWRSVETSGVAEEEATSGLVMLCIHGSLVNSYTNTPYTGALGLL
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von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ORF1, ORF2 & ORF3.
ORF3.
Viruses: SSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Pred. No. 1.8e-212;
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InterPro; IPR004261; SP2.
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"Sequence analysis of full length HEV clones derived directly human liver in fulminant hepatitis E.";
(In) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
VIRAL HERATITIS AND LIVER DISEASE, pp. 313-316,
Edizioni Minerya Andica, Torino (1997).
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EMBL; X98292; CAA66937.1; -.
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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GO; GO:0005198; F:structural molecule .
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InterPro; IPR008975; Viral_cap_coat.
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01-JAN-1998 (TrEMBLrel.
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Structural protein.
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      PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                          PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
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MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
Varacw. S.A., Binn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis E virus isolates from Egypt.J. Med. Virol. 57:68-74(1999).
EMBL, AF051352; AA035764.1;
GO: GO:0005198; F.structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR004261; SP2.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 5.1e-212;
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Hepatitis E virus.
Viruses; ssRNA positive-strand viruses,
Hepatitis E-like viruses.
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98.8%;
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Matches 652; Conservative
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   the EMBL/GenBank/DDBJ databases.
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MEDLINE=22072932; PubMed=12076829;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                   98.7%; Score 3362; DB 12;
98.8%; Pred. No. 1.1e-211;
ive 0; Mismatches 8;
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                                                                          70798 MW; A04C0185ACC085DB
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Submitted (MAR-1998) to the EMBL/GenBa
EMBL, AF051830; AAC97188.1;
GO; GO:0005198; F:structural molecule
Interbro; IPR004261; SP2
Interbro; IPR008275; Viral_cap_coat.
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Hepatitis E-like viruses.
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Capsid protein.
Hepatitis E virus.
                                                              Pfam; PF03014; SP2; 1.
SEQUENCE 660 AA; 70
                                                                                                                Similarity
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MEDLINE=9904-9628; PubMed=9833882;
Gouvea V., Snellings N., Popek M.J., Longer C.F., Innis B.L.;
"Hepatitis E virus: complete genome sequence and phylogenetic
     999
   Length
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OSMILLA:

O1-NOV-1999 (TrEMBIrel. 12, Created)

O1-NOV-1999 (TrEMBIrel. 12, Last sequence update)

O1-OCT--2003 (TrEMBIrel. 25, Last annotation update)

Capsid protein.

Hepatitis E virus.

Hepatitis E like viruses; no DNA stage;

Hepatitis E-like viruses.
  Score 3367; DB 12;
Pred. No. 5.1e-212;
4; Mismatches 6;
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SEQUENCE FROM N.A.
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                                                                                                                                                         Jameel S.;
"An Indian strain of hepatitis E virus (HEV): cloning, sequence, and expression of structural region and antibody responses in sera from individuals from an area of high-level HEV endemicity.";
J. Clin. Microbiol. 33:2653-2659(1995).
                                                                                            STRAIN=HYDERABAD;
MEDLINE=96087204; PubMed=8567900;
Panda S.K., Nanda S.K., Zafrullah M., Ansari I.H., Ozdener M.H.,
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                                                                      SEQUENCE FROM N.A.
Hepatitis E-like .
NCBI_TaxID=12461;
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    hepatitis E virus based of following long RT-PCR.";
                                                                                                                                                                                                                                                                                                                          629;
                                                                                                                                                                                                                                                                                                                   98.1%; Score 3342.5; DB 12; Length 98.3%; Pred. No. 2e-210; Live 1; Mismatches 9; Indels
                                                                                     SEQUENCE FROM N.A.
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Submited (DEC-2001) to the EMBL/GenBank/DDBJ databases.
ENBL; AF459438; AAM66330.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PP03014; SP2; 1.
SEQUENCE 659 AA; 70842 MW; ABCC177EBE6012C8 CRC64;
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Viruses; ssRNA positive-strand viruses, no DNA stage;
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"Reevaluation of a North India isolate of
the full-length genomic sequence obtained
Virus Res. 86:53-58(2002).
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.3
Matches 649; Conservative
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61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                                       615 LAPHSALAALEDIVDYPARAHTFDDFCPECRILGLGGCAFQSIVAELGRLKKKKKKTRE 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takahashi K., Kang J.-H., Ohnishi S., Hino K., Mishiro S.;
"Genetic Heterogeneity of Hepatitis E Virus Recovered from Japanese Patients with Acute Sporadic Hepatitis.";
J. Infect. Dis. 185:1342-1345(2002).
BMBL, AB074918; BAB96562.1;
GO; GO:005198; Fistructural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR004975; Viral_cap_coat.
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                                                                                                                                                                                                                                                                                                                                                                             DNA stage;
                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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SEOUENCE 660 AA; 70980 MW; 19233C22F3E57FF8
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Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                 Created)
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STRAIN-JKN-Sap;
MEDLINE-21996248; PubMed-12001054;
                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
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Matches 607; Conservative
                                                                                                                                                                                                                      PRELIMINARY;
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Mishiro S.;
                                                                                                                                                                                                                                                                                                                           ORF2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takahashi K., Kang J.-H., Ohnishi S., Hino K., Mishiro S., "Genetic Heterogeneity of Hepatitis E Virus Recovered from Japanese Patients with Acute Sporadic Hepatitis.",

J. Infect. Dis. 185:1142-185:1002).

EMBL, AB074915; BAB96557.1; -.

GO, GO:0005198; F:structural molecule activity; IEA.

Interpro, IPR004261; SP2.

Pfam, PR03014; SP2; 1.

SEQUENCE 674 AA; 72591 MW; 5C196112F81A2265 CRC64;
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                                                                                                                                                                                                                    DNA stage;
                                                                                                                              Last sequence update)
Last annotation update)
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Hepatitis E-like viruses.
NCBL_TaxID=12461;
                                                                                                          Created)
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MEDLINE=21996248; PubMed=12001054;
                                                                                                     01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
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es 607; Conservative
                                                               PRELIMINARY;
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Submitted (NOV-2001)
                                                                                                                                                                                             Hepatitis E virus.
                                                                                                                                                                                                                                                                                 [1] = SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         STRAIN=JAK-Sai;
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Search completed: August 16, 2004, 13:35:04 Job time : 43 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein August 16, 2004, 13:33:52; Search time 19 Seconds (without alignments) 1793.323 Million cell updates/sec Run on:

1 MRPRPILLLLLLMFLPMLPAP......QSTVAELQRLKMKVGKTREL 660 US-09-851-410A-8 3408 Perfect score: Seguence:

BLOSUM62 Scoring table:

389414 seqs, 51625971 residues Gapop 10.0 , Gapext 0.5 Searched: 389414

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cgn2 6/ptodata/2/iaa/5A COMB.pep:*
2: /cgn2 6/ptodata/2/iaa/5B COMB.pep:*
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6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Appl	Appl	Appl	Appl	Appli	Appl	Appli	Appl	Appli	Appl	Appl	Appl	Appli	Appl	Appli	Appli	Appli	Appl	Appl	Appli	Appli	Appl:	Appl	Appl	Appl	Appl	Appl
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence
SUMMAKIES	ID	US-08-240-049B-15	US-08-259-148A-19	US-08-484-054-19	US-07-876-941A-19	US-08-478-507-8	US-08-542-634-13	-128-	US-08-477-292-13	US-09-553-427-8	US-09-462-606-50	US-07-870-985A-19	PCT-US95-13703-13	US-09-172-699-2	US-09-462-606-12	US-08-840-316-2	US-08-809-523-2	8	US-09-462-606-49	US-09-462-606-56	US-09-402-776-2	PCT-US93-08849A-2	PCT-US93-08849-2	US-09-462-606-51	US-09-462-606-52	US-09-462-606-53	US-09-462-606-55	US-09-462-606-54
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3221 94.5 3221 94.5 3194.5 94.3 3194.5 93.7 3194.5 93.7 3194.5 93.7 3194.5 93.7 3194.5 93.7 3164.5 93.7 3164.5 93.7 2865 84.1 2813 82.8 2813 82.5 2813 82.5 2813 82.5 2813 82.5 2813 82.5 2813 82.5 2814 82.5 2815 82.5	ĸ	Ŋ	4	Н	Н	Н	N	m	4	4,	4	4	m	m	Ŋ	m	ഗ	m
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	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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APPLICANT: Reyes, Gregory R. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. TITLE APPLICANT: Yarbough, Patrice O. NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis E Virus (Burma strain)
ORF-2
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORTWRE: BACENTIN Release #1.0, Version #1.25
SOGTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION NUMBER: 38,615
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                Sequence 15, Application US/08240049B Patent No. 5686239 GENERAL INFORMATION:
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STATE: CA
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MOLECULE TYPE: I
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US-08-240-049B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-240-049B-15
                                                                                                                                                                                                                                                                                                             COUNTRY:
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. 0 0 Query Match 100.0%; Score 3408; DB 1; Length 660; Best Local Similarity 100.0%; Pred. No. 3.7e-294; Matches 660; Conservative 0; Mismatches 0; Indels 0;

1 MRPRPILLLILMFLPMLPAPPPGQPSGRRRGRRSGGSGGFWGDRVDSQPFAIPYIHPTN 60

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100.0%; Score 3408; DB 1; Length 660;
Best Local Similarity 100.0%; Pred. No. 3.7e-294;
Matches 660; Conservative 0; Mismatches 0; Indels 0
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                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
PRIOR APPLICATION NUMBER: US 822,335
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 0.5-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FRIING DATE: 1.5-CT-1989
PRIOR APPLICATION NUMBER: US 367,486
FRIING DATE: 1.6-UN-1989
PRIOR APPLICATION NUMBER: US 36,672
FRIING DATE: 1.6-UN-1989
PRIOR APPLICATION NUMBER: US 208,997
FRIING DATE: 1.7-UN-1988
ATTORNEY AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCZION NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 660 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
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PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
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                                                                                 PFAPDVTAAAGAGPRVROPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP
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APPLICANT: Bradley, Daniel W.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Yam, Albert W.
APPLICANT: Xarbough, Patrice D.
APPLICANT: Yarbough, Patrice D.
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
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STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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               TOPOLOGY:
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                                                                                                                                      DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIOOYSKTFFVLP
                                                          LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                     Sequence 19, Application US/08484054

Patent No. 5770689

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reyes, Daniel W.
APPLICANT: Taw, Ur-Shin
APPLICANT: Taw, Albert W.
APPLICANT: Taw, Albert W.
APPLICANT: Taw, Albert W.
APPLICANT: Heavezynski, Krzysztof Z.
ITILE OF INKTAWCZYNSKi, Krzysztof Z.
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 4600-0093.38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-4UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION DATA:

APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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US-08-484-054-19
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| Patent No. 5885768
| GENERAL INFORMATION |
| APPLICANT: Reves, Gregory R. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Mitchell, Carl |
| TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and TITLE OF INVENTION: Antibodies |
| VORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Deblinger & Associates |
| STREET: 350 Cambridge Avenue, Suite 250 |
| CITY: Palo Alto
                                                                                                                                                                                              Length 660;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                          100.0%; Score 3408; DB 1;
100.0%; Pred. No. 3.7e-294;
ive 0; Mismatches 0;
                                                                                                  ORF 2, BURMA, FIGURE
                                                                                                                                                                                                                                                     Matches 660; Conservative
MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                           ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                           Best Local Similarity
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481 DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yarbough, Fallic.
APPLICANT: Bradley, Daniel W
APPLICANT: Brawczynski, Krzysztof Z
APPLICANT: Tam. Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enterically Transmitted
TITLE OF INVENTION: No. 6120988-A/No. 6120988-B Hepatitis Viral Agent
541 IRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGFVSISAVAV
                                                                   VGEIGRGIALTLFNLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ
                                                                                                                                                       QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
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: 350 Cambridge Avenue, Suite 250
Palo Alto
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-UUN-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
RILING DATE: 16-UUN-1989
FRIOR APPLICATION DATA:
FILING NAMER: US 07/336.677
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
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11-APR-1989
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Yarbough, Patrice O
Bradley, Daniel W
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APPLICANT: Reyes,
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                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
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INDIVIDUAL ISOLATE: ORF 2, BURMA, FIGURE 9
US-07-876-941A-19
                                                                                                                                                                                                                                                                                                                                         PALOX APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 36,7486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 206,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 206,997
FILING DATE: 17-JUNE-1988
APPLICATION NUMBER: US 206,997
FILING DATE: 17-JUNE-1988
                                                                            COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palcal
                                                                                                                                                                                                                    FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
RIOR APPLICATION DATA:
FILING DATE: 17-DAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
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amino acid
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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61 PFAPDVTAAAGGGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                  THEREFOR
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ORF-2
                                                                                                                                                                                                                                                                                           SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTONEN'AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE (415) 324-0860
TELEFRANCE (415) 324-0860
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEBATITIS E VIRUS ANTIGENS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 3408; DB 3;
100.0%; Pred. No. 3.7e-294;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          660 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 660; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-542-634-13
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                                                                                                                                                       STATE: CA
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                                              NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE DOCKET NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPRAN: (650) 324-0860
INFORMATION FOR SEQ 1D NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
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Patent No. 6214970
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: McAkee, C. Patrick
APPLICANT: Yarbough, Patrice O.
                                                                                                                                                                              ....IRRISTICS:
TYPE: amino acids
TOPOLOGY: lin-
          17-JUN-1988
                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-478-507-8
                                                                                                                                                                                                                                                                                                                                                          Similarity
          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        Local Simi
hes 660;
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US-08-542-634-13
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LENGTH: 660 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                       Best_Local Similarity 100.
Matches 660; Conservative
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STATE: CA
COUNTRY: US
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                                                                      US-09-128-275A-8
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                                                                                                                                                                             Sequence 8, Application US/09128275A
Patent No. 6229005
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patrice O
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: No. 6229005-A/No. 6229005-B Hepatitis Viral Agent
                     DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                         481 DQSTYGSYTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                      LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTUTE: IBM PC compatible
COMPTUTE: IBM PC compatible
COMPTUTE: IBM PC compatible
COMPTUTE: IBM PC compatible
COMPTUTE: IBM PC compatible
SOFTWARE: Patentil Release #1.0, Version #1.25
SOFTWARE: Patentil Release #1.0, Version #1.25
SOFTWARE: Patentil Release #1.0, Version #1.25
FILING DATE: 03-AMG 1998
PRIOR APPLICATION NUMBER: US 08/279,823
FRILNG DATE: 25-AUL.1994
FRILNG DATE: 15-APR:1991
FRILNG DATE: 05-APR:1991
FRILNG DATE: 05-APR:1990
FRILNG DATE: 10-APR:1989
FRILNG DATE: 13-ACT:1989
FRILNG DATE: 13-ACT:1989
FRILNG DATE: 13-ACT:1989
FRILNG DATE: 16-AUN.1989
FRILNG DATE: 16-AUN.1989
FRILNG DATE: 16-AUN.1989
FRILNG DATE: 16-AUN.1989
FRILNG DATE: 16-AUN.1989
FRILNG DATE: 11-AUN.1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 324-0800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 07/208,997
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APPLICATION NUMBER: US 07
FILING DATE: 17-JUN-1988
ATTORNEY/AGENT INFORMATION:
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61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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; Sequence 13, Application US/08477292
; Patent No. 6291641
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; Patent No. 6291641
; Patent No. 6291641
; Patent No. 6291641
; Patent No. 629
                                                                                                                             0;
Length 660;
                                                                                                                             Indels
100.0%; Score 3408; DB 3; 100.0%; Pred. No. 3.7e-294;
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480 480

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601 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLQGCAFQSTVAELQRLKMKVGKTREL 660
       541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600
                                                                                                                                                                                                                                                                           APPLICANT: Reyes, Gregory R
APPLICANT: Yarbough, Patrice O
APPLICANT: Yarbough, Patrice O
APPLICANT: Standley, Daniel W
APPLICANT: Krawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
APPLICANT: Fry, Kirk E
APPLICANT: Fry, Kirk E
APPLICANT: Fry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Pry, Kirk E
APPLICANT: Palo Alto
CORRESPENDIBLE APPLICATION: No. 6379891-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE APPLICATION: Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/no/err
FILING DATE.
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FILING DATE: 07-UN-1995
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-UU-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION NUMBER: US 07/420,921
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER:
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FILING DATE: 16-UNN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
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Patent No. 6379891
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TELECOMMUNICATION INFORMATION
TELEPHONE: (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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TOPOLOGY:
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STATE:
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ORF-2
                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3408; DB 3;
Pred. No. 3.7e-294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,952
                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 NAME: Brookes, Allan A
REGIETRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G32PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)369-9500
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
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Best Local Similarity
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                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                               FILING DATE
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241 ASELVIPSERLHYRNQGMRSVETSGVAEEEATSGLVMLCIHGSLVNSYINTPYTGALGLL 300
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                                                                                                                              PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120
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                                                                  MRPRPILLLLLMFLPMLPAPPGQPSGRRRGRRSGGSGGGFWGDRVDSQPFAIPYIN
                                     ó
      Length 660;
                                     Indels
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Patent No. 6455492
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Ur-Shin
APPLICANT: Twu, Jr-Shin
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INFORTION: Hepatitis E Virus Vaccine and
      Score 3408; DB 4;
Pred. No. 3.7e-294;
0; Mismatches 0;
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350 Cambridge Avenue, Suite
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
         100.0%;
Query Match
Best Local Similarity 100.
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STREET: 350
CITY: Palo
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                                          Gaps
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Sequence 50, Application US/09462606

Patent No. 6432408

GENERAL INFORMATION:
APPLICANT: MENG, XIANG-JIN
APPLICANT: Berson, Suzanne U.
APPLICANT: Emerson, Suzanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: A SWINE HEPATITIS E VIRUS AND USES THEREOF
FILE REFERENCE: 20264251031
CURRENT APPLICATION NUMBER: US/09/462,606
CURRENT PILING DATE: 2000-06-12
PRIOR FILING DATE: 1997-07-18
PRIOR PILING DATE: 1997-07-18
PRIOR PILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 65

SOFTWARE: PATENTING UNIVER: 1998-07-17
SOFTWARE: PATENTING UNIVER: 2.1
SOFTWARE: PATENTING UNIVER: 2.1
SOFTWARE: PATENTING UNIVER: 2.1
SEQ ID NO 50
LENGTH: 660
                                          0
            Length 660;
                                          Indels
         100.0%; Score 3408; DB 4;
100.0%; Pred. No. 3.7e-294;
ive 0; Mismatches 0;
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CRGANISM: Hepatitis E virus
US-09-462-606-50
        Query Match
Best Local Similarity 100.
Matches 660; Conservative
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US-09-462-606-50
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                       QDKGIAIPHDIDLGESRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY
                                                                                                     DOSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
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ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND TITLE OF INVENTION: USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 3408; DB 5; 100.0%; Pred. No. 3.7e-294;
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STREET: P.O. Box 60850
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application PC/TUS9513703 GENERAL INFORMATION:
APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFRENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
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STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                  PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fabian, Gary R. 33,875
REGISTRATION UNDBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                            FILING DATE: 20-APRIL-1992
CLASSIFICATION:
                                                                                                                              APPLICATION DATA:

FILING DATE: 17-JAN-1992

RIOR APPLICATION NUMBER: US 505,888

FILING DATE: 05-APRIL-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 420,921

FILING DATE: 13-OCYOBER-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 367,486

FILING DATE: 16-UNE-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 336,672

FILING DATE: 11-APRIL-1989

PROR APPLICATION DATA:

APPLICATION NUMBER: US 208,997
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:
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                SOFTWARE: Patentin Rel.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Best Local Similarity 100.
Matches 660; Conservative
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                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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QY         121 PVPDVDSRGAILERQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180           DD         121 PVPDVDSRGAILERQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS 180           QY         181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI 240           DD         181 NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTPTSVDMNSITSTDVRILVQPGI 240           CQY         241 ASELVIPSERLHYRNQGMRSVETGGVAEERATSGLVMLCTHGSLVNSYTNTPYTGALGLL 300           DD         241 ASELVIPSERLHYRNQGMRSVETGGVAEERATSGLVMLCTHGSLVNSYTNTPYTGALGLL 300           DD         241 ASELVIPSERLHYRNQGMRSVETGGVAEERATSGLVMLCTHGSLVNSYTNTPYTGALGLL 300	301 DFALELEFRNITPGNINTRVSRYSSTARHRIRRGADGTAELTITAATREMKDLYFTSTNG 301 DFALELEFRNITPGNINTRVSRYSSTARHRIRRGADGTAELTITAATREMKDLYFTSTNG 301 DFALELEFRNITPGNINTRVSRYSSTARHRIRRGADGTAELTITAATREMKDLYFTSTNG 361 VGEIGRGTALTLENLADTLLGGLPTELISSAGGQLFYSRPVVSANGEPTVKLYTSVENAQ	TAAEY TAAEY TAAEY FFVLP FFVLP	QY         541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600           Db         541 LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGPVSISAVAV 600           Cb         601 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLGCCAPQSTVAELQRLXMKVGKTREL 660           Cb         601 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLGCCAPQSTVAELQRLXMKVGKTREL 660           Cb         601 LAPHSALALLEDTLDYPARAHTFDDFCPECRPLGLGCGCAPQSTVAELQRLXMKVGKTREL 660	RESULT 13 US-09-172-690-2 ; Sequence 2, Application US/09172699A ; Patent No. 6514690 ; GENERAL INFORMATION: ; APPLICANT: Anderson, David A. ; APPLICANT: Locarnini, Stephen A. ; APPLICANT: Locarnini, Stephen A. ; APPLICANT: Li, Fan ; APPLICANT: Li, Fan ; APPLICANT: Li, Fan ; TILLE OF INVENTION: IMMUNORBACTIVE ANTIGENS OF HEPATITIS E VIRUS ; FILE REPERENCE: Davies Col. Cave ; CURRENT APPLICATION NUMBER: US/09/172,699A ; CURRENT FILING DATE: 1996-10-14 ; EARLIER PILING DATE: 1996-06-20 ; NUMBER OF SEQ ID NOS: 24 ; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 2 ; LENGTH: 660 ; TYPE: PRT ; ORGANISM: Homo sapiens	Query Match         99.7%; Score 3399; DB 4; Length 660;           Best Local Similarity         99.7%; Pred. No. 2.38-293;           Matches 658; Conservative 1; Mismatches 1; Indels 0; Gaps 0;           Qy         1 MRPRPILLLLMFLPMLPAPPPGQPSGRRRGRRSGSGGGFWGDRVDSQPFAIPYIHPTN 60           Db         1 MRPRPILLLLMFLPMLPAPPPGQPSGRRRGRRSGSGGGFWGDRVDSQPFAIPYIHPTN 60           Qy         61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLATAVAPAHDTP 120           Db         61 PFAPDVTAAAGAGPRVRQPARPLGSAWRDQAQRPAVASRRRPTTAGAAPLTAVAPAHDTP 120

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completed: August 16, 2004, 13:36:07
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PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
                     PVPDVDSRGAILRRQYNLSTSPLTSSVATGTNLVLYAAPLSPLLPLQDGTNTHIMATEAS
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                                               NYAQYRVARATIRYRPLVPNAVGGYAISISFWPQTTTTFTSVDMNSITSTDVRILVQPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
APPLICANT: Esarev, Sergei. A., and Robinson, Robin A.
TITLE OF INVENTION: Recombinant Proteins Of
TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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STATE: NEW YORK
STATE: NEW YORK
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US-08-840-316-2
US-08-840-316-2
; Patent No. 6054567
; GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Richard W. Bork
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                     Indels
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Pred. No. 7.6e-292;
2; Mismatches 3;
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TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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TYPE: amino acid acid sTRANDEDNESS: unknown
""DOILOGY: unknown
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.2
Matches 655; Conservative
                                                                                                                                                                                     US-08-840-316-2
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// Search time 51 Seconds
(without alignments)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                      August 16, 2004, 13:35:07
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0
seq length: 200000000
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                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Result No.	7	7	c.	4	S	9	7	80	σ	10	11	12	13	14	15

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1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2

## ALIGNMENTS

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APPLICANT: Fuerst, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fabian, Gary R.
REGISTRATION UNDERE: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/542,634
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 13:
                      Sequence 13, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
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US-09-769-066-13
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US20030124510A1-A/No. US20030124510A1-B Hepatitis Vira
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No. 7.9e-276;
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                                                                       STREET: 350 Cambridge Avenue, Suite CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,410
FILING DATE: 07-May-2001
PRICATION NUMBER: US/09/851,410
PRICATION NUMBER: 09/128,275
FILING DATE: CADADOMN:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
APPLICATION NUMBER: US 07/420,921
FILING DATE: 10-APR-1990
APPLICATION NUMBER: US 07/420,921
FILING DATE: 10-CT-1989
APPLICATION NUMBER: US 07/367,486
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/36,672
FILING DATE: 11-APR-1989
APPLICATION NUMBER: US 07/306,672
FILING DATE: 11-ADN-1988
ATTORNEY, ARCHAUT ON NUMBER: US 07/208,997
FILING DATE: 11-ADN-1988
ATTORNEY, ARCHAUT ON NUMBER: US 07/208,997
FILING DATE: 11-ADN-1988
                                                            Associates
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MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-851-410-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Petithory, Joanne R. REGISTRATION NUMBER: 42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                          ADDRESSEE: Dehlinger &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
    No.
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Best Local Similarity 100.
Marches 660; Conservative
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                                                      STRANDEDNESS: Hepatitis E Virus (Burma strain) ORF-2
                                                                                                                                                                                                                                 Score 3408; DB 9;
Pred. No. 7.9e-276;
; Mismatches 0;
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                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: NO
ONIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-769-066-13
                      LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                          0:
                                                                                                                                                                                                                                   100.0%;
ilarity 100.0%;
Conservative 0
    SEQUENCE CHARACTERISTICS:
                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                       Similarity
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Best Local Simi
Matches 660;
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Sequence 1, Application US/10381770
Publication No. US20040052813A1
GENERAL INFORMATION.
APPLICANT: YANG SHENG TANG company, Ltd.
APPLICANT: TANG SHENG TANG COMPANDION: COMPRISHED FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOSITIVE OF INVENTION: COMPRISHING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REFERENCE: IECO10037PCT
CURRENT APPLICATION NUMBER: US/10/381,770
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                                                                                                                                                                                          ORF 2, BURMA, 2 ID NO: 19:
TELEPHONE: (415) 324-098
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
                                                                                                                                                                                    ; SEQUENCE DESCRIPTION: SEQUES-868-19
                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                 TYPE: amino acid
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US-10-381-770-1
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFCATION OATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary R. REGISTRATION UNBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
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FILING DATE: 16-UNR-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNB-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
TWU, Dregory R.
TWU, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
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US-10-165-868-19
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/ No. US20030220475Ale
OTHER INFORMATION: Synthetic construct
US-10-257-044-1
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MCAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HPPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                          660;
                                                                                                                                                                                                                                          Length
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                                                       4.0
PRIOR APPLICATION NUMBER: 60/195,380 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 LENGTH: 660
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Patent No. US20020107360A1
GENERAL INFORMATION:
                                                                                                                          ORGANISM: Artificial Sequence
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Publication No. US20030220475A1
Publication No. US20030220475A1
Publication No. US20030220475A1
Publication No. US20030220475A1
Publication No. US20030220475A1
Publication No. US20030220475A1
APPLICANT: The Government of the United States of America, as APPLICANT: Howard A. FIELDS
APPLICANT: Howard A. FIELDS
APPLICANT: JIHONG MENG
APPLICANT: JIHONG MENG
TITLE OF INVERTION: NEUTRALIZING IMMUNOGENIC HEV POLYPEPTIDES (HEV)
FILE REFERENCE: 14114.034902
CURRENT APPLICATION NUMBER: US/10/257,044
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                                                                                                                                                                   660;
                                                                                                                                                                   Length
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                                                                                                                                                             Score 3391; DB 12;
Pred. No. 2.1e-274;
1; Mismatches 3;
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   2003-07-16
                                                                                                                                                             Query Match
Best Local Similarity 99.4%;
Matches 656; Conservative
                                                                                                           ORGANISM: hepatitis E virus
CURRENT FILING DATE: 2003-
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version
SEQ ID NO 1
                                                                        099
                                                                                                                            US-10-381-770-1
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                                                                                            TYPE: PRT
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421 QDKGVAIPHDIDLGDSRVVIQDYDNQHEQDRPTPSPAPSRPFSVLRANDVLWLSLTAAEY 480
                                                             DQSTYGSSTGPVYVSDSVTLVNVATGAQAVARSLDWTKVTLDGRPLSTIQQYSKTFFVLP
                                                                                                                                                                                       LRGKLSFWEAGTTKAGYPYNYNTTASDQLLVENAAGHRVAISTYTTSLGAGFVSISAVAV
                                                                                                                                                                                                                       541 LRGKLSFWEAGTTKAGYPYNYNTTASDQILIENAAGHRVAISTYTTRLGAGPVAISAAAV
                                                                                      Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Isloppy disk
COMPUTER: PPC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
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STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
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APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUME-1989
APPLICATION NUMBER: US 336,672
APPLICATION NUMBER: US 336,672
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APPLICATION NUMBER: US 208,997
FILING DATE: 17-UWB-1988
ATTORNEY/AGENT INFORMATION:
NAME: FADIAN, GALY R.
REGISTRATION NUMBER: 33,875
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TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                                                                                                                                                                                             COMPUTER KEADABLE FORM:

MEDIUM TYPE: COMPATIBLE
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION INTRER: US/09/769,066
FILING DATE: 4-Jan-2001
CLASSIFICATION: <university control of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible of the compatible 
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Best Local Similarity 93.5%; Pred. No. 3.4e-260;
Matches 617; Conservative 21; Mismatches 22;
                         ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-769-066-14
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LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                                                                                ZIP: 94306
COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                   COUNTRY:
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Sequence 51, Application US/10239090A

Publication No. US20040101820A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FULL APPLICANT: KABUSHIKI KAISHA TOSHIBA

TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/239,090A

CURRENT APPLICATION NUMBER: US/10/239,090A

CURRENT APPLICATION NUMBER: J02001-191837

WUMBER OF SEQ ID NOS: 57

SEQ ID NOS: 57

LENGTH: 660
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                                674;
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                                                              Indels
                              93.3%; Score 3179; DB 16; 92.1%; Pred. No. 1.1e-256;
                                                              25; Mismatches
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                                               Best Local Similarity 92.19
Matches 607; Conservative
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US-10-239-090A-57
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| Publication No. US20040101820A1
| Publication No. US20040101820A1
| GENERAL INFORMATION:
| APPLICANT: KABUSHIKI KAISHA TOSHIBA
| TITLE OF INVENTION: from Japanese, chip including the same, kit including the same,
| TITLE OF INVENTION: from Japanese, chip including the same, kit including the same,
| TITLE OF INVENTION: detecting hepatitis E virus using the same,
| TITLE OF INVENTION: DATE: 2003-07-24
| CURRENT PELICATION NUMBER: US/10/239,090A
| PRIOR APPLICATION NUMBER: JP2001-191837
| PRIOR APPLICATION NUMBER: JP2001-191837
| NUMBER OF SEQ ID NOS: 57
| SEQ ID NO 57
| TYPE: PRT
| TYPE: PRT
| TYPE: PRT
| TYPE: PRT
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Pred. No. 5.6e-258;
1; Mismatches 24; DB
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SEQUENCE DESCRIPTION: SEQ ID
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                                               US-10-165-868-20
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US-10-239-090A-55
; Sequence 55, Application US/10239090A
; Publication No. US20040101820A1
; GENERAL INFORMATION:
; APPLICAMY: KABUSHIKI KAISHA TOSHIBA
; TITLE OF INVENTION: from Japanese, chip including the same, rithe OF INVENTION: detecting hepatitis E virus using the same
; TITLE OF INVENTION: detecting hepatitis E virus using the same
; TITLE OF INVENTION: detecting hepatitis E virus using the same
; CURRENT APPLICATION NUMBER: US/10/239,090A
; CURRENT FILING DATE: 2003-07-24
; PRIOR PILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 57
; EDECTHE OF SEQ ID NOS: 57
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larity 92.0%; Pred. No. 1.4e-255;
Conservative 24; Mismatches 29;
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US-10-239-090A-55
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Sequence 53, Application US/10239090A
Sequence 53, Application US/10239090A
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Sequence 53, Application US/1020A
Sequence 53, Application US/1020A
Sequence 53, Application US/1020A

GENERAL INFORMATION:
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92.1%; Pred. No. 2.9e-256;
iive 25; Mismatches 27;
  Pred. No. 2e-256;
; Mismatches 26;
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607; Conservative 26;
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Matches 607; Conservative
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US-10-239-090A-53
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APPLICANT: ADDOTT Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Desai, Suresh M.
APPLICANT: Desai, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: MARANARY: I. K.
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HOWBER: US/10/319,745
CURRENT FILING DATE: 2002-12-13
FRIOR PAPLICATION NUMBER: US/09/468,147A
PRIOR PILING DATE: EABLIER FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/061,199
PRIOR PILING DATE: EARLIER FILING DATE: 1991-10-15
NUMBER OF SEQ ID NOS: 258
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DB 10;
Query Match 92.7%; Score 3160; DB 10; Best Local Similarity 91.7%; Pred. No. 4.3e-255; Matches 604; Conservative 27; Mismatches 28;
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APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Brker, James C.
APPLICANT: Brker, James C.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Watshawar, I. K.
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION NUMBER: US 09/173,141
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1997-10-15
EARLIER FILING DATE: 1997-10-15
SEALIER FILING DATE: 1997-10-15
SEALIER FILING DATE: 1997-10-15
SEQUID NO 92
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FEATURE:
OTHER INFORMATION: Xaa = Unknown or Other at
OTHER INFORMATION: Xaa = Unknown or Other at
OTHER INFORMATION: Xaa = Unknown or Other at
US-09-468-147-92
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FILE REFERENCE: 6232.US.P1
CURRENT APPLICATION NUMBER: US/09/468,147A
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER FILING DATE: 1998-10-15
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEO ID NOS: 258
SOFTWARE: FASTERO FOR WINDOWS Version 3.0
SEO ID NO 167
                                                                                                                                                                    Other
Other
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                                                                                                                                                                   OTHER INFORMATION: Xaa = Unknown or OTHER INFORMATION: Xaa = Unknown or US-09-468-147-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 167, Application US/10319745
Publication No. US20030211467A1
GENERAL INFORMATION:
                                                                                                                                  TYPE: PRT
ORGANISM: Hepatitis E Virus
FEATURE:
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APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Deasi, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
APPLICANT: MISHAHWAR, I. K.
APPLICANT: WHINDIN: HEPAITIDS E VIRUS
                                                                         OTHER INFORMATION: Xaa = Unknown or Other at position 481 OTHER INFORMATION: Xaa = Unknown or Other at position 542 OTHER INFORMATION: Xaa = Unknown or Other at position 595 US-10-319-745-92
                                                                                                                                                         Indels
                                                                                                                                                         28;
                                                                                                                                  DB 12;
                                                                                                                                 92.7%; Score 3160; DB 12; 91.7%; Pred. No. 4.3e-255;
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          3.0
         Windows Version
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                                                    ORGANISM: Hepatitis E Virus
                                                                                                                                            Best_Local Similarity 91.73
Matches 604; Conservative
        SOFTWARE: FastSEQ
SEQ ID NO 92
LENGTH: 660
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Pred. No. 2.4e-254;
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Matches 603; Conservative 26; Mismatches
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APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION HEPATITIS E VIRUS
TITLE OF INVENTION NUMBER: US/09/468,1478
CURRENT FILING DATE: 1999-112-13
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US 60/061,199
PRIOR FILING DATE: EARLIER FILING DATE: 1999-10-15
PRIOR PLING DATE: EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Mindows Version 3.0
SERVICE TO 167
LENGTH: 660
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Best Local Similarity 91.5%; Pred. No. 2.4e-254;
Matches 603; Conservative 26; Mismatches 30;
                  Schlauder, George G.
Erker, James C.
Desai, Suresh M.
   APPLICANT: Abbott Laboratories
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Aar96103 |
Aar70323 |
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 Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cqqq2 1/V3PTO spool p/USO9851410/runat 16082004 125716 9617/app query.fasta_1.4238
-Q=/Cqqq2 1/V3PTO spool p/USO9851410/runat 16082004 125716 9617/app query.fasta_1.4238
-DB=A Geneseq 29Jan04 -QFMT=fastan -SUFFIX=oli.rag-MINMATCH=0.1 -TGOPCL=0
-LOOPEXT=0 -UNITGS=bits -STRAT=1 -END=-1 -MATRIX=oligo -TRAMS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM==ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRE-USO9951410 @CGN 1 1.141 @runat 16082004 125716 9617 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -SOFBLCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Aar56089 Hepatitis
Aaw35826 Hepatitis
Aaw80197 Protein e
Aaw93389 Human HEV
Aab52233 HEV-Burma
Aao15699 Hepatitis
Add24376 Hepatitis
                                                                                                      August 16, 2004, 13:35:43 ; Search time 89.8179 Seconds (without alignments) 12476.164 Million cell updates/sec
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                                                                                                                                                                                                    1 ATGCGCCCTCGGCCTATTTT.....GTAAAACTCGGGAGTTGTAG 1983
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             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                          - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                282547505 residues
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Ygapext 60.0
Fgapext 7.0
Delext 7.0
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AAR39306

AAR96089

AAW35826

AAW30197

AAB24120

AAB24120

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2011s:*
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geneseqp2003as:*
geneseqp2003bs:*
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seq length: 200000000
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Ygapop 60.0 , Y
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Result No No

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TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020
                                                                                                                             GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAAATGCTCAG
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                                                                                                                                                                                       GInSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu
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TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla
                        ATTTCCACTTACACCACTAGCCTGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
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HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                                                                                     Hepatitis E virus (HEV) antigens derived from ORP 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
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                                                                                                                                                                                                                                                                              Yarbough
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                                                                                                                                                                                                                                                                                                            GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu
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                                               GTCGGTGAGATCGGCCGCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                  361 ValGlyGlulleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAaAspThrLeuLeu
                                                                                                            GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCGTCCC
                                                                                                                                                                      GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
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                   LeuThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGly
                                                                                                                                                                                                                                 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGTTATT
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TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaAlaGlyHisArgValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr
                                                                                                                                  CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG
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                                                           GITAATGITGCGACCGCGCGCGCGCTTGCCCCGGTCGCTCGATTGGACCAAGGTCACA
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890S-00367486.
890S-00420921.
900S-0050888.
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                          ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr
                                                                                            GCTGTCGGCGGTTACGCCATCTCCATCTCTGGCCACAGACCACCACCACCCGACG
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                                                                            TCTCCCCTTACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCCTCTT
                                                                                                                                                  AGTCCGCTTTTACCCCTTCAGGACGCCACCAATACCCATATAATAGGCCACGGAAGCTTCT
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A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with a HEV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents the protein from the open reading frame, ORF2, from HEV Burma strain. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HEV, specifically the HEV Burma and Mexico strains. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
                                                Diagnosis of hepatitis E virus Burma and Mexico strain infection - by immunoassay with hepatitis E virus peptide antigens.
                                                                                                                          Disclosure; Col 39-42; 36pp; English.
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Alignment Scores:			
Pred. No.:	0	Length:	099
Score:	00.099	Matches:	099
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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qq	1 MetAr	MetArgProArgProlleLeuLeuLeuLeuLeuMetPheLeuProMetLeuProAlaPro 20
Ολ	61 CCGCC	CCGGTCAGCCGTCTGGCCGCCGTCGTGGGCGGCGGCGGCGGCGGTTCCGGCGG
Dβ	21 ProPr	ProProGlyGlnProSerGlyArgArgArgGlyArgArgSerGlyGlySerGlyGlyGly 40
ò	121 TTCTG	GGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA
Dp	41 PheTr	PhetrpGlyAspArgValAspSerGlnProPheAlalleProTyr1leHisProThrAsn 60
ò	181 CCCTT	CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGGCTGGACTCGTGTTCGCCAACCCGCC 240
ΩÞ	61 ProPh	ProPheAlaProAspValThrAlaAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla 80
δλ	241 CGACC	CGACCACTCGGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGT 300
Db	81 ArgPr	
λ̈	301 AGACC	AGACCTACCACAGCTGGGGCCGCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCG 360
QQ	101 ArgPr	oThrThrAlaGlyAlaAlaProLeuThrAlaValAlaProAlaHisAspThrPro 120
ά	361 CCAGT	CCAGTGCCTGATGTCGACGCCGCGGCGCCATCTTGCGCCGGCAGTATAACCTATCAACA 420
QQ	121 ProVa	ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140
λ̈́	421 TCTCC	TCTCCCCTTACCTCTTCCGTGGCCACCGCCACTAACCTGGTTCTTTATGCCGCCCCTCTT 480
DÞ	141 SerPr	oleuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProLeu 160
٥'n	481 AGTCC	AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540
ДD	161 SerPr	oleuLeuProLeuGlnAspGlyThrAsnThrHislleMetAlaThrGluAlaSer 180
λ	541 AATTA	AATTATGCCCAGTACCGGGTTGCCCGTGCCAAATCCGTTACCGCCCGC
ΩÞ	181 AsnTy	AsnTyrAlaGinTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsn 200
ολ	601 GCTGT	GCTGTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACAGACCACCACCACCGACG 660
dO ,	201 Alava	AlaValGiyGiyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 220

o O O	661	TCCGTTGAIATGAAITCAATAACCTCGACGGAIGTTCGTAITTTAGTCCAGCCCGGCATA 720 
රු සි	721	IGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 78
ò	781	GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGGGGCTACCTCTCTGGTTATGCTTTGCATA 840
Dp	261	ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 280
λ	841	CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 900
DÞ	281	HisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu 300
දු ද	901	GACTITGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCGGTAACACCAATACGCGGGTC 960  L[
ે ઠે	961	TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020
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۵⁄	1021	CICACCACAGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080
QQ	341	LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGly 360
<i>&amp;</i>	1081	GTCGGTGAGATCGGCCGCGGGATAGCCCTGCTCGACCTTGCTGACTCTCTGTT 1140
qq	361	ValGlyGlulleGlyArgGlyLleAlaLeuThrLeuPheAsnLeuAaAspThrLeuLeu 380
<i>ا</i> م	1141	GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTCGCCCGTCTCTACTCCCGTCCC 1200
QQ	381	GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPro 400
٥x	1201	GTIGICICAGCCAAIGGCGAGCGACTGTTAAGTIGTATACATCIGTAGAGAATGCTCAG 1260
Dβ	401	ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGlu 420
δ	1261	CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320
οp	421	GinaspLysGlyIlealaileProHisAspIleAspLeuGlyGluSerArgValValIle 440
δλ	1321	CAGGATTATGATAACCAACAIGAACAAGAIGGGCGGACGCCTTCTCCAGCCCCAICGGGC 1380
Db	441	GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 460
δ	1381	CCTTTCTCTGTCCTTCGAGCTAATGATGCTTTGGCTCTCTCT
Db	461	ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 480
δλ	1441	GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 1500
Ωp	481	AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 500
٥٨	1501	GTTAATGTTGCGACCGGGCGGCGGTTGCCCGGTCGCTCGATTGGACCAAGGTCACA 1560
Dþ	501	ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 520
٥٧	1561	CTIGACGGICGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCG 1620
Пр	521	LeuaspGlyargProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro 540
٥x	1621	CTCCGCGGTAAGCTCTCTTTCTGGGAGGCACACACTAAAGCCGGGTACCCTTATAAT 1680
Ωp	541	LeuargglyLysLeuSerPheTrpGluAlaglyThrThrLysAlaglyTyrProTyrAsn 560
٥y	1681	TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGGGCGCGCGC
Db	561	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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                                                          CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC
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              TTAGCCCCCCATTGCGTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCTGCCCGCGCC
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Burma HEV isolate; vaccine; diagnostic
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Hepatitis E virus; HEV;
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(revised)
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11-APR-1989;
16-JUN-1989;
13-OCT-1989;
05-APR-1990;
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25-MAR-2003
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Pred. No.:
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Human HEV ORF 2 protein from strain Burma

(first entry)

11-JUN-1999

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ValGlyGlulleGlyArgGlyIleAlaLeuThrLeuPheAsnLeuAlaAspThrLeuLeu
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                                      CTCACCACCACGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
                                                                                        GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
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mutants which are capable of cross reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in vaccines for immunishing against HEV infection. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used as a therapeutic treatment for infection by other antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a swine hepatitis E virus (HEV) and its natural
                                                        therapy;
                                                                                                                                                                                                                                                                                                                                            New isolated swine hepatitis E virus - used to develop products for th diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans.
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                                                      hepatitis E virus, HEV; cross-reaction; antibody; human; le; immunise; infection; detection; diagnosis; prevention.
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Gaps:
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                                                                                                     Hepatitis E virus.
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241 CGACCACTCGGCTCCGCTTGGCGTGACCAGGCCCCAGCGCCCCGCCGTTGCCTCACGTCGT 300

ProPheAlaProAspValThrAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla

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standard; protein; 660

AAW93389

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SAXAX

Db 441 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 460  Qy 1381 CCTTTCTCTGTCCTTCGAGCTAATGATGTTTTGGCTCTCTCT		18 60 62 62	QY         1861 CATACTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC         1920           DD         621 HisThrPheAspAspPheCysProGluCysArgProLeuGlyLeuGlnGlyCysAlaPhe         640           QY         1921 CAGTCTACTGCTGGCTTCAGGCCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG         1980           DD         641 GlnSerThrValAlaGluLeuGlnArgLuysWetLysValGlyLysThrArgGluLeu         660	SULT 7 924120 AAB24120 standard; protein; 660 AA. AAB24120; 29-JAN-2001 (first entry)	DE Hepatitis E virus Burma strain ORF2 protein sequence SEQ ID NO:8.  XX  KW Hepatitis E virus; HEV; non-A/non-B viral hepatitis; viral protein;  KW immunological; diagnosis; hepatitis; infection; identification;  KW vaccine; immunoreactive; hepatotropic; antiinflammatory; virucide;  XX  Hepatitis E virus.		
ArgproleuglySerAlaTrpArgAspGlnAlaGlnArgproAlaValaSerArgArg ArgproLeuglySerAlaTrpArgAspGlnAlaGlnArgproAlaValaSerArgArg ArgproLeuglySerAlaTrpArgAspGlnAlaGlnArgproAlaValaSerArgArg ArgproCargCacGacGacGacGacGacGacGacGacGacGacGacGacGa	481 AGITCGCTTTTACCCCTTCAGACGGGCACCAATACCCATATAATGGCTGGGAGGTTCT 540  [	AlavaldiydiytyzAlaileSerileSerPheltpProGlintrhrthrThrFrontr 2 TCGTTGATATGAATTCAATAACCTCGACGAATGTTCGTATTTTAGTCCAGCCCGCCTA 7 TCGTTGATATGAATTCAATAACCTCGACGAATGTTCGTATTTTAGTCCAGCCCGCATA 7 ServalAspMetAsnSerIleThrSerThrAspvalArgIleLeuvalGlnProGlyIle 2 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACCTATCGTAACCAAGGCTGGCGCTCC 7	241 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 260 781 GTCGAGACCTCTGGGGTGGCTGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840 [		1021 CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080	1141 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCGGCTGTTCTACTCCCGTCCC 1200	ValvalSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 420 CaGGATAAGGGTATTGCAATCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 132 [

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GENELABS TECHNOLOGIES INC. US GOVERNMENT.
(GENE-) (USGO)
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Reyes GR; Tam A, Bradley DW, Yarbough PO, Krawczynski KZ, Fry KE, WPI; 2000-593712/56.

N-PSDB; AAA99259

Identifying recombinant antigen immunoreactive with antibody induced by hepatitis E virus (HEV), for detecting HEV infection, comprises immunoreacting a polypeptide from an HEV genome with an HEV-positive antiserum.

Claim 6; Col 63-68; 46pp; English.

The present invention describes a method for identifying a recombinant antigen immunoreactive with a hepatitis B virus (HEV)-induced antibody. The method comprises producing a polypeptide derived from an HBV genome, immunoreacting the polypeptide with an HBV-positive antiserum and selecting the polypeptide as a recombinant antigen if the polypeptide reacts with the HBV-positive antiserum. The method is useful for identifying recombinant antigen immunoreactive with antibody induced by HBV. The enterically transmitted non-A/non-B hepatitis (ET-NANB (also known as HBV))-specific fragments are useful for identifying ET-NANB. Who contain additional sequence information, as primers for detecting ET-NANB viral genomic material in a patient sample, for the synthesis of polypeptides for use in immunoassays, and for identifying synthesis of polypeptides for use in immunoassays, and for identifying strains, the antigens are especially useful in the preparation of vaccine against ET-NANB infection. These antigens may further be used to prepare antibodies to ET-NANB virus particles for use directly as antiviral agents, and to produce antiserum designed for pre- or post-exposure prophylaxis. The present sequence represents a specifically claimed HEV Burma strain protein sequence for use in the present invention

Sequence 660 AA

is Similarity: 100.00% Maches:  Match: 3 Gaps: 3 Gaps: 3	Alignment Scores: Pred. No.:	0	Length:	099
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: 100.00% 3	Local Similarity:	100.00%		0
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		3	Gaps:	0

Db	121	ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140
δλ		rcccrtacctctrccgrggccaccggcactaaccrggrrcrtrargccgccccrtr
Dp		erProleuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyrAlaAlaProleu 16
0y	481	GCTTTTACCCCTTCAGGACGACCAATACCCATATAATGGCCACGGAAGCTTCT 5
qa	161	SerProLeuLeuProLeuGlnAspGlyThrAsnThrHisileMetAlaThrGluAlaSer 180
٥y	541	AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC
qa	181	AsniyrAlaGlniyrArgValAlaArgAlaThrileArgTyrArgProLeuValProAsn 200
٥٨		GCTGTCGGCGGTTACGCCATCTCCATCTCGGCCACAGACCACCACCCCCGACG 660
ф		AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 220
ð i	9	TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720
q _Q		SerValAspMetAsnSerIleThrSerThrAspValArgIleLeuValGlnProGlyIle 240
ð í		GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780
a	4	AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 260
ð í	ا ف	GTCGAGACCTCTGGGGTGGCTGAGGAGGGGGCTACTCTGGTCTTGTTATGCTTTGGATA 840
gg	261	ValGluThrSerGlyValAlaGluGluGluHaThrSerGlyLeuValMetLeuCyslle 280
රි සි	841	CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG 900
2	0	nibelyoetueuvalasioetiyiiiitasiiiiiFiOiyiiiiiGiyalabeuciybeabeu 300
ò	0	GACTITIGCCCTTGAGCTTTGGGTTTCGCAACCTTACCCCCGGTAACACGCAATACGCGGGTC 960
qq	301	AspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgVal 320
à	961	TCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGAGCGGGACTGCCGAG 1020
qq	321	srArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu 3
ζ	1021	4
QQ	341	LeuThrThrThrAlaAlaThrArgPheMetLysAspLeuTyrPheThrSerThrAsnGly 360
ŏ	1081	٦
Ор	361	3
λŏ	1141	SECTGCCGACAGAATTGATTTCGTCGGCTGGCCAGCTGTTCTACTCCCGTCCC
Db	381	GlydlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlyGlbLeuPheTyrSerArgPro 400
٥٨	1201	STCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
Db	401	4,
0y	1261	13
DD	421	GinaspLysGlyIleAlaileProHisAspIleAspLeuGlyGluSerArgValVallle 440
ζζ	1321	М
QQ	441	GINASPITYTASDASNGINHISGIUGINASPARGPTOThrProSerProAlaProSerArg 460
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qq		roPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr
ò	1441	AGTOCACTTATGGCTCTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 15
QQ	481	31nSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu

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The invention relates to an isolated DNA comprising the genome of an referrically transmitted nonA/nonB (ET-NANB) viral hepatitis agent (also referred as HEV). The DNA sequences or their fragments are useful in preparing ET-NANB viral proteins and as probes for virus detection. These are particularly useful in diagnosing infection by an enterically transmitted agent (e.g. ET-NANB virus), as well as in vaccine production. The Present sequence represents a ORF2 protein encoded by a ET-NANB viral DNA sequence from HEV-Burma strain
  in vaccine production.
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  (e.g. ET-NANB virus),
                                    Disclosure; Col 63-68; 45pp; English
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                                    GTTAATGTTGCGACCGCGCGCGCGCGTTGCCCCGGTCGCTCGATTGGACCAAGGTCACA
                                                                                            CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACTTCTTTGTCCTGCCG
                                                                                                                    TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
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N-PSDB; AAF83495.
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ET-NANB; infectio
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The invention comprises a method for detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in a sample and isolating HEV agents or nucleic acid fragments produced by the agent. The method utilises PCR - using bile from a human or cynomolgus monkey actively infected with HEV as a source of the agent. The method of the invention is used for detecting the presence of a viral agent in a sample of cultured cells infected with the agent and isolating enterically transmitted nonA/nonB HEV agents or nucleic acid fragments produced by the agent. The present amino acid sequence represents the protein encoded by open reading frame 2 (ORF2) of a DNA sequence isolated from a Burmese strain of the Hepatitis E virus
                                                                                         CAGICIACIGICGCIGAGCIICAGCGCCIIAAGAIGAAGGIGGGIAAAACICGGGAGIIG 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting the presence of enterically transmitted nonA/nonB hepatitis viral (HEV) agents in bile samples from infected humans and monkeys using polymerase chain reaction.
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                                                                                                                                                                                                                                                                          transmitted nonA/nonB hepatitis viral agent;
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Matches:
Conservative:
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                                         CATACTTTTGATGATTTCTGCCCCAGAGTGCCGCCCC
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89US-00336672.
89US-00420921.
90US-0050888.
91US-00681078.
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Burma strain; bile; ORF2
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St Local Similarity: 100.00%   Mismatches: 0   Indels: 0	Proclycintroserciyargargargargargserciysiyserciyciyciy TGGGGTGACCCTTCGCAATCCCTATATTCATCCAACCAAC	241 CGACCACTCGCTTCGCGTGACCAGCCCCGCCCTGCCGTTGCTCACTGTCTTGTCTTACTGTTGTCTTACTCTCACTCTCTTGCGTTGCTTGTCTTACTGTCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	361 CCAGTGCCTGATGTCGACTCCGGGGGCCATCTTGCGCGGCAGTATAACCTATCAACA 42	Oy 481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540	601 GCTGTCGGCGGTTACGCCATCTCCATCTCGGCCACAGACCCACCACCCCCGACG 66	Qy         721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGCGCGCTCC 780           Db         241 AlaSerGluLeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer 260           Qy         781 GTCGAGACCTCTGGGGGGGGGGGGGGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840           Db         261 ValGluThrSerGlyValAlaGluGluAlaThrSerGlyLeuValMetLeuCysIle 280	Qy         841 CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGGCTGCTCGGGCTGTTG         900           Bb         281 HisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu         300           Qy         901 GACTTTGCCCTTGAGCTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC         960           Db         301 AspPheAlaLeuGluPheArgAsnTrGCAACCAACTGCTGGGGTC         960           Qy         961 TCCCGTTATTCCAGCACTGCTCGCCGCCTTCGTCGCGGGTCGGGACGGGACTGCCGGG         1020           Qy         961 TCCCGTTATTCCAGCACTGCTCGCCCCCCCCTTCGTCGCGGGCGCGGGACGGGACTGCCGGG         1020           Db         321 SerArgTyrSerSerThrAlaArgHisArgLeuArgArgClyAlaAspGlyAlaAspGlyThrAlaGlu         340

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                                                                                                                                                                                                                                                                                                                                                                                                                                    New proteins derived from an enterically transmitted non-A/non-B (ET-NANB) viral hepatitis agent, useful for diagnosing ET-NANB infection and producing vaccines for immunizing an individual against ET-NANB hepatitis viral agent.
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Matches:
Conservative:
Mismatches:
Indels:
                              HEV;
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                              hepatitis; ET-NANB;
 Burma ORF
                                                            Burma
                                                                                                                                                                             88US-00208997.
89US-00336672.
89US-00420921.
90US-0050588.
91US-0061078.
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virus strain
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N-PSDB; ADD24374.
                                                            Hepatitis E virus;
                              non-A/non-B viral
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                                                                                         US2003124510-A1
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                                                                                                                                                                             17-JUN-1988;
11-APR-1989;
13-CVT-1989;
05-APR-1990;
05-APR-1991;
25-JUL-1994;
03-AUG-1994;
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This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible
                                                                                                                                                                                                                                                            ProvalProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr
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Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, immuno-assays and nucleic acid hybridisation.
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                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                         Claim 13; Page 24-26; 29pp; Japanese
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Query Match:
DB:
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         ProPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr
                                                                                           CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG
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                                         GACCAGICCACTIAIGGCICTICGACIGGCCCAGITIAIGITICIGACICIGIACCTIG
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N-PSDB; AAV61688.
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                                                                ValValSerAlaAsnGlyGluProThrValLysELeuTyrThrSerValGluAsnAlaGln
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                                                       GCCGCCTGCCCACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC
                                                                                             GITGICICAGCCAATGGCGAGCCGACTGITAAGITGIAIACAICTGIAGAGAATGCICAG
                                                                                                                                CAGGATAAGGGTATTGCAATCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT
                                                                                                                                                                                GInAspTyrAspAsnGlnHisGluGInAspArgProThrProSerProAlaProSerArg
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62K antigen (AAR96091) comprises the C-terminal 549 amino acids of hepatitis E virus (HEV) Burma strain capsid protein (see also AAR96089). It is obtd. by PCR amplification of HEV Burma ORF-2 (AAT27107), insertion of amplified DNA (AAT27109) into vector pGBX and expression in B. colls. Expression of full-length ORF-2 in Sf9 insect cells using a baculovirus system also results in prodn. of 62K antigen (see also AAR96103). 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                                                    Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines
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                                                                   CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953
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/note= "This region contains P1-P51 overlapping synthetic
peptides"
                                                                                                                                                                                                                                                                                                                                                                                                                                    C-terminal portion of the pORF2 protein of hepatitis E virus polypeptide containing a neutralizing epitope, useful to detect, prevent and treat hepatitis E virus infections.
CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAG
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Percent Similarity: Best Local Similarity:

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DNA (AAT27109) coding for the 62K antigen (AAR96091) of hepatitis E virus (HEV) Burma strain capsid protein was cloned into baculovirus expression vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells. High levels of expression were obtd, and the recombinant 62K was obtd. in over 95% purity. However, C-terminal processing resulted in the deletion of 9 or 23 amino acids from 62K, giving 2 related polypeptide species (AAR96101 and AAR96103). Similar results were obtd. with HEV Mexico 62K antigen (see also AAR96102 and AAR96104). Recombinant 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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        nbv; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                                                                                                                                                                                                                                                                                                                                   antigens derived from ORF 2 - useful as determining HEV infection and in vaccines.
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                                                                                Burma strain
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95US-00542634.
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101 1 694 G	rpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120 TTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA 753	
21 V		
754 C 141 H	CACTATCGTAACCAAGGCTGGGGGTCCGTCGAGACCTCTGGGGGTGGCTGAGGAGAGGCT 813 	
814 A       T	ACCICTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACA 873 	
874 C   181 P	CCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTT 933	
934 A       201 T	ACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCCACCGCCTT 993 	
994 C	CGTCGCGGTGCGGACCGGACTGCCGAGCTCACCACGGCTGCTACCCCGCTTTATGAAG 1053 	
1054 G	GACCTCTATTTTACTAGTACTAATGGTGTGGGGGGGTCGGCGGGGGGATAGCCCTCACC 1113 	<del></del>
1114 C	CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT 1173 	
1174 G     281 G	GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCACCAATGGCGAGCCGACTGTTAAG 1233 	
1234 T	TTGTATACATCTGTAGAAATGCTCAGCAGGATAAGGGTATTGCAATCCGCATGACATT 1293 	
1294 G     321 A	GACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGATAACCAACAACAAGATCGG 1353 	
1354 C       341 P	CCGACGCCTTCTCCAGCCCCATCGCGCCCTTTCTCTGTCCTTCGAGCTAATGATGTGCTT 1413 	
1414 T	GGCTCTCTCTCACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCA 1473 	
1474 G 381 V	GTTTATGTTTCTGACTCTGGACCTTGGTTAATGTTGCGACCGGGGCGCAGGCCGTTGCC 1533 	
1534 C       401 A	CGGTCGCTCGATTGGACCAAGGTCACACTTGACGGTCGCCCCCTCTCCACCACCACGCGG 1593 	
1594 T     421 T	TACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGC	
1654 A	ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713 	
1714 G 461 G	GAGAATGCCGCCGGGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGT 1773 	

1774 CCCGTCTCCATTTCTGCGGTTGCCGTTTTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAG 1833	481 ProValSerileSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGlu 500	1834 GATACCTTGGACTACCCTGCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC 1893	501 AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg 520	1894 CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953	521 ProLeuGlyLeuGlnGlyCysAlaPheGlnSerThrValAlaGluLeuGlnArgLeuLys 540
1774 CCCGTCTCCATTTCTGCGC	481 ProvalSerIleSerAlav	1834 GATACCTTGGACTACCCTC	501 AspThrLeuAspTyrPro	1894 CCCCTTGGCCTTCAGGGCT	521 ProbeuGlyLeuGlnGlyC
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Search completed: August 16, 2004, 13:47:46 Job time: 126.818 secs

RIAMR Sheet

protein search,

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Scoring table:

Title: Perfect score:

Sequence:

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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B44212 VHWWHE C44212 B40236 B86242 T12281

660 659 123 123 41 337 348 840

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Query Match

Result No. 100.0 18.2

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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                             using frame_plus_n2p model
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Ωp	401	  ValValSe				420
ογ	1261	CAGGATAA	GGGTATTGCAATCCC	GCATGACATTGACCTC	GGAGAATCTCGTGTGGTTATT	1320
qq	421	GlnAspLy	sGlylleAlallePr		GInAsplysGly1leAla1leProHisAsplleAspLeuGlyGluSerArgValVallle	440
& a	1321	CAGGATTA	TGATAACCAACATG! 	ACAAGATCGGCCGACC	CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC	1380
ò	1381	CCTTTCTC	TGTCCTTCGAGCTAA	TGATGTGCTTTGGCT(	TCTCTCACCGCTGCCGAGTAT	, <del>(</del>
qa	461	 ProPheSe				480
à i	1441	GACCAGTO	CACTTATGGCTCTTC	CGACTGGCCCAGTTTAI	GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG	1500
a ;	481	AspGlnSe	rThrTyrGlySerSe	erThrGlyProValTy:	ValSerAspSerValThrLeu	00
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ð	1561	CTTGACGG	TCGCCCCTCTCCAC	CATCCAGCAGTACTCC	CTTGACGGTCGCCCCTCTCCACCATCCAGGAGTACTCGAAGAACCTTCTTTGTCCTGCCG	1620
d	521	LeuAspGl	yArgProLeuSerTk	ırlleGlnGlnTyrSeı	LysThrPhePheValLeuPro	40
상 음	1621	CTCCGCGG         	TAAGCTCTCTTTCTC 	GGAGGCAGGCACAACT 	CTCCGCGGTAAGCTCTTTCTGGGAGGCAGGCACAAACTAAAGCCGGGTACCCTTATAAT 	1680 560
δ	1681	TATAACAC	CACTGCTAGCGACCA	ACTECTTGTCGAGAAT	GCCGCGGGCACCGGGTCGCT	1740
qa	561	TyrAsnTh		nLeuLeuValGluAsr		580
δλ	1741	ATTTCCAC	TTACACCACTAGCCT	GGGTGCTGGTCCCGTC	ATTICCACTIACACCACIAGCCIGGGGGGGCGCCGTCCCATTICIGGGGTGCCGTT	1800
qq	581	lleSerTh	rTyrThrThrSerLe	uGlyAlaGlyProVal	SerlleSerAlaValAlaVal	009
ò	1801	TTAGCCCC	CCACTCTGCGCTAGC	ATTGCTTGAGGATACC	TTAGCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCCC	1860
ΩP	601	LeuAlaPr	oHisserAlaLeuAl	aLeuLeuGluAspThr	LeuAspTyrProAlaArgAla	620
රු අ	1861	CATACTTT	TGATGATTTCTGCCC 	AGAGTGCCGCCCCTT	CATACTITIGATGATITCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTCTC	1920 640
ä	,					
ර් යි	1921	CAGT 	TGTCGCTGAGCTTCP               rValAlaGluLeuGl	GCGCCTTAAGATGAAG 	CTACTGTCCCTGACCTTCAGCGCCTTAAGATGAAGGTGGGTAAAACTCGGGAGTTG 	1980 660
RESULT 2 B44212 Structural C;Species: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 C;Date: 17 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0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-1994 #sc 0-	RESULT 2 B44212 CSPECIAL STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE 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Oy 122 TCTGGGGTGGACCGGGTTGATTCTCAGCCCTTCGCAATCATCATCCAACCCAGCC 181  Db 55 SerGlyValThrGlyLeulleLeuSerProSerGlmSerProllePheileGlnProThr 74  Oy 182 CCTTGGCCCCGGTGCGGCGGCGGGGGGCTGGTTCGCCACCCGCC 241  Db 75 ProSerProProMetSerProLeuArgProGlyLeuAspLeuValPheAlaAsnProPro 94  Oy 242 GACCACTGGGCTCGCTTGGCCGGCGGGGGCGGGGGTGGCTGGC	Alignment Scores:     4.45e-51	Oy 182 CCT 184          75 Pro 75            75 Pro 75            75 Pro 75
Dercent Similarity: 100.00\$   Mismatches: 0   Ouery Match: 18.18\$   Indels: 0   Ouery Match: 18.18\$   Indels: 0   Ouery Match: 18.18\$   Indels: 0   Ouery Match: 18.18\$   Indels: 0   Ouery Match: 18.18\$   Indels: 0   Ouery Match: 18.18\$   Ouery Match: 18.18\$   Ouery Match: 18.18\$   Ouery Match: 18.18\$   Ouery Match: 18.18\$   Ouery Match: 18.18\$   Ouery Match: 19.18\$   Ou	Cippecies: hepatitis E virus (strain Burma) Cippecies: hepatitis E virus Cippecies: hepatitis E virus Cippecies: hepatitis E virus Cippecies: hepatitis E virus Cippecies: bepatitis E virus Cipacession: B40778; A40236 R;Tam, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G. Virology 185, 120-131, 1991 Virology 185, 120-131, 1991 Virology 185, 120-131, 1991 A;Reference number: A40778; MUID:92024067; PMID:1926770 A;Accession: B40778 A;Molecule type: genomic RNA A;Residues: 1-123 crpMs A;Residues: 1-123 crpMs A;Cross-references: GB:M73218; NID:g330023; PIDN:AAA45735.1; PID:g330025 A;Title: Indian hepatitis E virus shows a major deletion in the small open reading frame A;Reference number: A40236; MUID:92295577; PMID:1534953 A;Accession: A40236 A;Molecule type: genomic RNA A;Residues: 1-57, "P; 59-1022 A;Molecule type: genomic RNA A;Residues: 1-57, "P; 59-1022 A;Molecule type: genomic RNA A;Residues: 1-57, "P; 59-1022 A;Molecule type: genomic RNA C;Superfamily: hepatitis E virus structural protein 1 C;Keywords: structural protein	Alignment Scores: Pred. No.: 2

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Unknown protein, 73054-77165 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hunge, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H96635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BH2230 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 0.1-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: F83928
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1091 <STO>
A;Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB05949.1; GSPDB:GN00
A;Experimental source: strain C-125
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AE005173; NID: g6751691; PIDN: AAF27674.1; GSPDB: GN00141
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                                                                      Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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A;Molecule type: DNA
A;Residues: 1-840 <STO>
                                                                                                                    Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                  Alignment Scores:
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Pred. No.:
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A;Gene: T7P1.16
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A;Description: Molecular phylogeny of a live-bearing fish genus Poecilia (Cyprinidontific A;Accession: T12281
A;Accession: T12281
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricession: B86242
Ritheologis, A.; Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Poecilia sphenops mitochondrion C;Species: mitochondrion Poecilia sphenops
C;Date: 23-Jul_1999 #sequence_revision 23-Jul-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF031390; NID:g2653584; PID:g2653585; PIDN:AAB87615.1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE005172; NID:g4874264; PIDN:AAD31329,1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                              337
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0
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1 4
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
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Matches:
Conservative:
Mismatches:
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A;Molecule type: DNA
A;Residues: 1-337 <STO>
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Query Match:
     C; Keywords: structural
                                                                                                                         Percent Similarity:
Best Local Similarity:
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Percent Similarity: Best Local Similarity:

Query Match: DB:

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A; Gene: BH2230

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US-09-851-410A-6

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Pypothetical protein NMB0903 [imported] - Neiseeria meningitidis (strain MC58 serogroup C;Species: Neisseria maningitidis
C;Species: Neisseria maningitidis
C;Accession: 10-14
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Caradi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
                                                                                                                                                                                                                                                                                                                                                           A;Accession: D81144
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <TET>
A;Cross-references: GB:AE002442; GB:AE002098; NID:g7226133; PIDN:AAF41311.1; PID:g722614
A;Experimental source: serogroup B, strain MC58
A;Gene: NMB0903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical 15K protein (hgiDIIM 3' region) - Herpetosiphon aurantiacus N.Alternate names: ORF15 (Species: Herpetosiphon aurantiacus C.Species: Herpetosiphon aurantiacus C.Species: Herpetosiphon aurantiacus C.Species: Herpetosiphon aurantiacus C.Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Mar-2000 (S.Accession: JT0593, S21948 M. A. Kroeger, M. A. Kroeger, M. A. A. Kroeger, M. A. Fritle: Cloning, sequence and characterization of m5C-methyltransferase-encoding gene, A. Recession: JT0592; MUID:92039068; PMID:1937045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-138 <DUES.
A,Cross-references: EMBL.X55141; NID:948771; PIDN:CAA38940.1; PID:948772
A,Experimental source: strain Hpa2
C,Superfamily: Herpetosiphon aurantiacus hypothetical 15K protein (hgiDIIM 3' region)
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64 ThrArgProGluValAlaSerSer
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S19708
hypothetical protein C - Herpetosiphon aurantiacus
C;Species: Herpetosiphon aurantiacus
C;Species: Herpetosiphon aurantiacus
C;Accession: S19708
R;Erdmann, D.; Duesterhoeft, A.; Kroeger, M.
Bur. J. Blochem. 202, 1247-1256, 1991
A;File: Cloning and molecular characterization of the HgiCI restriction/ modification A;Reference number: S19706, MUID:92111503; PMID:1662609
A;Accession: S19708
                                                                                                                                                                                                                                                                                                                                                                                                   protamine II - black rat snake (fragment)
C;Species: Elaphe obsoleta quadrivittata
C;Species: Slaphe obsoleta quadrivittata
C;Accession: HS8208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, J. Biol. Chem. 271, 2547-2557, 1996
A;Tile: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
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Length:

A;Residues: 1-41 <HUN> C;Superfamily: sperm histone A; Molecule type: protein A; Residues: 1-41 <HUN>

A;Status: preliminary A; Accession: H58208

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Best Local Similarity:

Query Match:

Percent Similarity:

Alignment Scores:

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Indels:

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Best Local Score:

Percent Similarity:

Alignment Scores: Pred. No.:

EMBL: X55138

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-74 <KRO> A;Cross-references: EM

827 ACAAGACCAGAGGTAGCCTCCTCC 804

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EXDV701R family protein [imported] - Caulobacter crescentus
C.Species: Caulobacter crescentus
C.Species: Caulobacter crescentus
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C.Species: Caulobacter crescentus
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C.Species: Caulobacter crescentus
R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; DeBoy, R.T.; Palorer, C.N.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87649
A;Accession: F87649
A;Accession: Palorer crescentus
A;Accession: Caulobacter crescentus
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-166 cARN>
A;Cross-references: GB:AE001711; GB:AE000512; NID:g4980788; PIDN:AAD35380.1; PID:g498079
A;Experimental source: strain MSB8
                                                                                                                         C;Accession: D72394
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: D72394
hypothetical protein TM0292 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A,Gene: TM0292
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P34554 Q13064 P18183

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Q13425 P37979 Q85fy6

Q64230 P27540 O02748

P53762 P41739

xylella fas xylella fas bradyrhizob

075173 P57972 Q9ph22 Q87f43 P30601

pasteurella

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sapien

homo homo homo

Q9h7z3 Q03164

drosophila

Q89186 P22265 Q96dn6

Searched:

Run on:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length viral genome.";
Virology 185:120-131(1991).
-!- FUNCTION: CONTENT A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92024067; PubMed=1926770;
MEDLINE=92024067; PubMed=1926770;
MEDLINE=92024067; PubMed=1926770;
MEDLINE=92024067; PubMed=1926770;
Mepatitis E virus (HEV): molecular cloning and sequencing of the
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5832A013CCC4A61C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Burma) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                               VST2_HEVBU STANDARD; PKI; bov AA. P29326.
P29326.
P29326.
P2932 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last noncation update)
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InterPro; IRR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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-MODEL=frame+ n2p.model -DEV=xlp
-G=Cgn2_1/USFTO_spool_p/US609851410/runat_16082004_125716_9625/app_query.fasta_1.4238
-G=Cgn2_1/USFTO_spool_p/US609851410/runat_16082004_125716_9625/app_query.fasta_1.4238
-D=SwissProt 42 -QFMT=fastan -SUFFIX=oli.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-USFRT=pto -UNITS=bits -START=1 -END=-1 -MATRIX=0.00000000
-USFRT=pto -NORM=ext -HEAFSIZE=500 -MINLEN=0 -MALIX=X=2000000000
-USFR=US09851410_@CGN_1 1_43_@runat_16082004_125716_9625_-NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALT -DSPBALCK=100 -LONGLOG
-DSW_TIMEOUT=120 -WARN TIMEOUT=30 -THERAD=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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                                                                          August 16, 2004, 13:36:13 ; Search time 18.2638 Seconds (without alignments)
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                    protein search, using frame_plus_n2p model
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Ygapop 60.0 , Y
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Result Ņ.

Oy 961 TCCCGTTATTCCAGCACTGCTCGCCGCTCGCGGTCGGACGGA	1141 GGCGGCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCGGCTGTTCTACTCCCGTCCC I GCGGCCTGTTCTACTCCCGTCCC I GLIGHT	CAGGATAAGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGTGGTTATT 1  [	1381 CCTTTCTGTCCTTCGAGCTAATGATGTCTTTGGCTCTCTCCCCGGTGCCCAGTAT 144 461 ProPheServalLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 480 1441 GACCAGTCCACTTATGGCTCTTCGACTGCCCCAGTTTTGTTTCTGACTGGCCTTG 150 1481 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrEeu 500	0y         1501 GTTAATGTTGCGACCGGCGCGCGTTGCCCGATTGCACCAAGGTCACA 1560           1	OY 1621 CTCCGCGGTAAGCTCTTTCTGGGAGGCACAACTAAAGCCGGGTACCCTTATAAT 1680	OY 1741 ATTTCCACTTACACCACTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT 1800	Oy 1861 CATACTTTGACCCAGAGTGCCCCCCTTGGCTTCAGGCTCCCCTTC 1920
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1008

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GACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTC 1188
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                                      GInProGly11eAlaSerGluLeuVal11eProSerGluArgLeuHisTyrArgAsnGln
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                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE=92115700, PubMed=1731327;
TSAIV S.A., Emerson S.U., Reyes G.R., TSAIRVA T.S., Legters L.J.,
Malik I.A., Igbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
"Characterization of a prototype strain of hepatitis E virus.";
"Characterization A Borotype STAIN OF HEATINGS";
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RN
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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STRUCTURAL PROTEIN 2.
8085BC53CF846FD3 CRC64;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Heparitis E virus (strain Pakistan) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Heparitis B-like viruses.
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Signal.
SIGNAL 1 22
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Best Local Similarity:
Query Match:
DB:
                                                                                                         NCBI TaxID=33774;
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Pred. No.:
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                                               172
81 ArgProLeuGlySerAlaTrpArgAspGlnAlaGlnArgProAlaValAlaSerArgArg 100
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                             AGACCTACCACAGAGCTGGGGCCGCCGCTAACCGCGGTCGCTCCGGCCCCATGACACCCCCG
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Rikihisa T., Mizuno
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                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
Structural protein 2 (Fragment).
Hepatitis E virus (isolate Rhesus) (HEV).
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Hepatitis E virus: cDNA cloning and expression."; Microbiol. Immunol. 36:67-79(1992).
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Uchida T., Suzuki K., Hayashi N., Iida F.
Wang C.-K., Shikata T., Ichikawa M., Riki
Win K.M.;
                                                                                                               CCAGTGCCTGATGTCGACTCCCGC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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Best Local Similarity:
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ID VST2_HEV
AC Q00270;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virus Genes 7:95-109(1993).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                      T., Ichikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST2_HEVMY (1-660)
                                                                                                          01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; ssNA, positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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CRC64;
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                                                                                                                                                                                                                                                                                  MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata
Rikihisa T., Winn K.;
                                                                                               660 AA.
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                  GCGGTTGCCGTTTTAGCCCCCCCCACTCT
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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SIGNAL
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                         243
                                                                                                                             790 TCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCA 849
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 CTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACC
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MEDLINE=92115700; PubMed=1731327;
Tastev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,
Malik I.A., Iqbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.",
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Hépatitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.";
Virology 185:120-131(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Burma;
MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST1_HEVBU (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02444; HEV ORF2; 1.
SEQUENCE 123 AA; 12676 MW; 8A5A798B1B74EDE5 CRC64;
                                                                                                                                                                                                                                                                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein I (ORF3).
Hepatitis E virus (strain Burma) (HEV), and
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                              viruses.
                                                                                                                                                                                                                                   STANDARD;
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NCBI_TaxID=31767, 33774;
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Query Match:
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                    ACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC
1093 GGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93079857; PubMed=1448913;
Huang C.C., Mguyen D., Rernandez J., Yun K.Y., Fry K.E.,
Bradley D.W., Tam A.W., Reyes GR.;
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    E virus (HEV).";
Virology 191:550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY RFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST2_HEVME (1-659)
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CF75E75EFD8FBE2C CRC64;
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Hepatitis E-like viruses.
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Last annotation update)
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InterPro; IPR004261; Sp2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
Signal.
1 22 RV GTWT1
                                                                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequ
01-FEB-1994 (Rel. 28, Last anno
Structural protein 2 precursor.
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70640 MW;
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VST2_HEVME
ID _VST2_HEV
AC _Q03500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 SerGlyValThrdlyLeulleLeuSerProSerGlnSerProllePhelleGlnProThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDINE=93079857; PubMed=1448913; Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E., Bradley D.W., Tam A. W., Reyes G.R.; "Molecular cloning and sequencing of the Mexico isolate of hepatitis
            CCCCCGATGTCACCGCTGCGCCTGGACCTCGTGTTCGCCAAC
                             Propromet SerProLeuArgProGlyLeuAspLeuValPheAlaAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST1_HEVME (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C888F5D638852A68 CRC64;
                                                                                                                                                                                         Hepatitis B virus (strain Mexico) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
NCBI_TaxID=31768;
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Mismatches:
Indels:
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                                                                                                                                 01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02444; HEV ORF2; 1.
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InterPro; IPR003384; HEV_ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M74506; AAA45731.1; -.
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61.00
100.00%
100.00%
9.24%
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                                                                                                                                                                              Structural protein 1.
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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              188
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                                                                                                                                                    GACCACTCGGCTCCGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGTA 301
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                                                                                                         GIGACCGGGTIGATICICAGCCCTICGCAATCCCCTATATICATCCAACCAACCCTTCG
                                               CTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCCGCGCGCCACCGCCCG
                                                                                         CCTTCGCCCCCGATGTCACCGCTGCGGCCGGGCTGGACCTCGTGTTCGCCAACCCGCCC
35 ArgProValSerArgLeuAlaAlaValValGlyGlyAlaAlaAlaValProAlaValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLLIBE-9222753; PubMed=8470371;
Aye T.T., Uczrida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-851-410A-6_COPY_5147_7129 (1-1983) x VST1_HEVMY (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR003384; HEV ORF2.
Pfam; PF02444; HEV ORF2; 1.
SEQUENCE 123 AA; 12751 MW; FB81143F0B31F8A4 CRC64;
                                                                                                                                                                                                                                                                                                                                  01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
01-0cT-1995 (Rel. 32, Last annotation update)
Structural protein 1 (ORF3).
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Mismatches:
Indels:
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Matches:
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76.00
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                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity:
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STRANS-C. Columbia;

MEDLINE=22954860; PubMed=14593172;

MEDLINE=22954860; PubMed=14593172;

Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

Rarlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Torlium M.J.,

Chan M.M., Tang C.C., Donodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 302:842-846(2003).
-!- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE P170 SUBUNIT OF
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=21125776; PubMed=11042177;
Burks E.A., Bezerra P.P., Le H., Gallie D.R., Browning K.S.;
Burks Initiation factor 3 subunit composition resembles mammalian initiation factor 3 and has a novel subunit.";
J. Biol. Chem. 276:2122-2131(2001).
translation initiation factor 3 subunit 3 (eIF-3 gamma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
                                 (eIF3 p38 subunit) (eIF3h).
TIF3H1 OR ATIG10840 OR T16B5.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:816-820(2000).
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                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE FROM N.A
                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
        Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                        factors
                                                                                                                                                                                                                                                                                                                        Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                              flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
-!- FUNCTION: Seems to be the binding site for several of the fact involved in protein synthesis and appears to be essential for accurate translation (By similarity).
-!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                                                                                                  Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein, Complete proteome.
SEQUENCE 121 AA; 12535 MW; 5AF9F83D2C94AC3E CRC64;
                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Solosomal protein L7/L12.
FPLL OR CPE2414.
                                121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00368; -; 1.

InterPro; IPR008332; Ribos_L12/7_olig.
InterPro; IPR00206; Ribosomal_L12.
InterPro; IPR00206; Ribosomal_L12.
IPRODOM; PD001326; Ribosomal_L12; 1.

TIGRFAMS; TIGR00855; L12; 1.
                                  PRT;
                                                                                                                                                                                                                                                                                      STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
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                                  STANDARD;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                            NCBI_TaxID=1502;
                                                                                                                                                                                                            Clostridium
                                RL7 CLOPE
Q8XHR7;
              RL7_CLOPE
RESULT 10
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EMBL; AF285833; AAG53614.1; -

SUBUNIT: eIF-3 is composed of at least 12 different subunits. SIMILARITY: Contains 1 MPN (JAB/Mov34) domain.

ACO07354; AAD31329.1; -. AY054641; AAK96832.1; -. AY081546; AAM10108.1; -. EMBL;

PIR; B86242; B86242. InterPro; IPR003639; Pept M67 Mov34. InterPro; IPR000555; Peptidase_M67.

Pfam; PF01398; Mov34; 1.

Probom; P0363422; Mov34 1; 1. SMART; SM00232; JAB_MPN; 1. Initiation factor; Protein biosynthesis.

V -> L (IN REF. 1). F9965DA546AC977C CRC64; 38372 MW; 337 AA; Alignment Scores: SEQUENCE

337 9 0 Conservative: Mismatches: Indels: Length: Matches: 4.89 9.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Query Match: US-09-851-410A-6_COPY_5147_7129 (1-1983) x IF33_ARATH (1-337)

Alignment Scores:

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STRAIN=137c / CC-125;
 Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
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P12852;
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                                                                                                                                                                                                                                                                                                                      MEDLINE=92039068; PubMed=1937045; Duesterhoeft A., Kroeger M., "Cloning, sequence and characterization of m5C-methyltransferase-encoding gene, hgiDIIM (GTCGAC), from Herpetosiphon giganteus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MRR-2004 (Rel. 43, Last annotation update)
3-isopropylmalate dehydratase small subunit 1 (EC 4.2.1.33)
[Isopropylmalate isomerase 1) (Alpha-IPM isomerase 1) (IPMI 1).
LEUDI OR TM0292.
                                                                                                                                                                                   01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 15.4 kDa protein in HgiDIIM 5 region (ORF15).
Herpetosiphon aurantiacus (Herpetosiphon giganteus).
Bacteria; Chioroflexi; Herpetosiphonales; Herpetosiphonaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-851-410A-6_COPY_5147_7129 (1-1983) x YD2M_HERAU (1-138)
                                                                               US-09-851-410A-6_COPY_5147_7129 (1-1983) x RL7_CLOPE (1-121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JT0593; JT0593.

Hyporchetical protein; Restriction system; DNA-binding.
DNA BIND
17
38
H-T-H MOTIF (POTENTIAL).
SEQÜENCE 138 AA; 15396 MW; E9CC70A0E11785A2 CRC64;
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           Matches:
Conservative:
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Mismatches:
                                  Mismatches:
                                                                                                                                                                        138 AA.
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                                                                                                                  ThrArgGlySerLeuLeuLeuSer 50
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8.00
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                  Best Local Similarity:
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Best Local Similarity:
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                       Percent Similarity:
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                                                                                                                                                                       YD2M HERAU
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                                             Query Match:
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 Pred. No.:
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                                                                                                                                                                        GERTARA
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                                                                                         STRAINS—MSB8 / DSM 3109 / ATCC 43589;
STRAINS—MSB8 / DSM 3109 / ATCC 43589;
MEDLINE—99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Catalyzes the isomerization between 2-isopropylmalate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and 3-isopropylmalate, via the formation of 2-isopropylmaleate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1989 (Rel. 12, Created)
1-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last amontation update)
Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isopropylmalate.
--- PATHWAY: Leucine biosynthesis; second step.
--- SUBUNIT: Heterodimer of leuC and leuD (By similarity).
--- SIMILARITY: Belongs to the leuD family. LeuD 2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-851-410A-6_COPY_5147_7129 (1-1983) x LED1_THEMA (1-166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: 2-isopropylmaleate + H(2)0 = 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP, MF 01032; -; 1.
InterPro, IPR000573; Aconitase_C.
Pfam, PF00694; Aconitase_C; 1.
Leucine biosynthesis; Lyses; Complete proteome.
SEQUENCE 166 AA; 18734 MW; D8ACF340205111A4 CRC64;
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001711; AAD35380.1; -.
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Pred. No.:
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                  S F F F W X X F F F S
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mayfield S.D., Schirmer-Rahire G., Frank H., Zuber H., Rochaix J.-D.; Analysis of the genes of the OBE1 and OBE3 proteins of the photosystem II complex of Chlamydomonas reinhardtii."; Plant Mol. Biol. 12:683-693 (1989).

-!- SUBCELDULAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.

-!- SIMILARITY: Belongs to the psbQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=96376499; PubMed=8781179; Choi G., Przybylska M., Straus D.; Three abundant germ line-specific transcripts in Volvox carteri encode photosynthetric proteins."; Curr. Genet. 30:347-355(1956).
-!- SUBCELLUIAR LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex.
-!- SIMILARITY: Belongs to the psbQ family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Volvocaceae, Volvox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3).
PSBO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLOROPLAST.
OXYGEN-EVOLVING ENHANCER PROTEIN 3.
8CCF077334CF79D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (1-199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-851-410A-6_COPY_5147_7129 (1-1983) x PSBQ_CHLRE
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Mismatches:
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Matches:
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16-OCT-2001 (Rel. 40, Last seq
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STRAIN=f. Nagariensis / HK10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X13832; CAA32061.1; -.
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InterPro, IPR008797, PsbQ.
Pfam, PF05757, PsbQ, 1.
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199
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STRAIN-ATCC 33913 / NCPEB 528;

REQUENCE FROM N.A.

STRAIN-ATCC 33913 / NCPEB 528;

MEDLINE-22022145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Berrollini M.C., Camargo L.E.B.,

A camarotte G., Cannavan F., Cardozo J., Chambergo F. Ciapina L.P.,

Rara J.B., Ferrala A.B., Fortala A.J.S., Perrellia R.C., Canton M.T.,

Rormighieri B.F., Franco M.C., Greggio C.C., Ferro M.I.T.,

Rormighieri B.F., Marchado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M. B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M. B.N., Mayaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.P.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Schubal J.C., Kitajima J.P.,

R. "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Plays a critical role in the incorporation of lipoproteins in the outer membrane after they are released by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lola protein (By similarity).
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                CHLOROPLAST (POTENTIAL).

OXYGEN-EVOLVING ENHANCER PROTEIN 3.

3103DDFC84CC3180 CRC64;
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                                                                            Pfan, PF05757; PsbQ; 1.
TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
Photosynthesis; Photosystem II; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-851-410A-6_COPY_S147_7129 (1-1983) x PSBQ_VOLCA (1-202)
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Mismatches:
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-!- SIMILARITY: Belongs to the lolB family.
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U22330; AAB40980.1; -.
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8.00
100.00%
100.00%
1.21%
                 PIR; S72224; S72224.
InterPro; IPR008797; PsbQ.
InterPro; IPR006311; Tat.
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                                                                                                                                             Thylakoid; Membrane.
IRANSIT
                                                                                                                                                                                    CHAIN 55
SEQUENCE 202 AA;
                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
Query Match:
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CR EMBL; AE012186; AAM40185.1; -.

DR HAWAP; MF 00233; -; 1.

DR InterPro; IPR00455; LolB

DR PFAM; PF03550; LolB.

DR PFAM; PF03550; LolB.

DR PFAM; PF03550; LolB.

DR PFAM; PF03550; LolB.

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21 21 N-Palmitar.

FT LIPID

22 21 N-Palmitar.

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23 21 N-Palmitar.

FT LIPID

24 32298 MW; 25A715B827CF782C CRC64;

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

DR No.0008 Conservative:

Query Match:

DR No.0008 Mismatches:

US-09-851-410A-6_COPY_5147_7129 (1-1983) x LOLB_XANCP (1-218)

DD 30 GlyAlaAlaProAlaValValGly 37
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Search completed: August 16, 2004, 13:48:43 Job time : 28.2638 secs

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MEDLINE-20271579; PubMed=10813471;
MEDLINE-20271579; PubMed=10813471;
Wan Cuvck-Gandre H., Zhang H.Y., Tsarev S.A., Warren R.L.,
Caudill J.D., Snellings N.J., Begot L., Innis B.L., Longer C.F.,
"Phylogenetically distinct hepatitis E viruses in Pakistan.";
Am. J. Trop. Med. Hyg. 62:187-189(2000).
EMBL; AR185822; AGG16766.1;
EMBL; AR185822; AGG16766.1;
InterPro; IPR008198; F:structural molecule activity; IEA.
InterPro; IPR008975; Viral_cap_coat.
Ffam; PF03014; SP2; 1.
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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Last annotation update)
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Q81871
Q9WLL4
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Q91169
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Hepatitis E virus.
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                                                   August 16, 2004, 13:39:23 ; Search time 97.0734 Seconds
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                                                                                                                                                                                                       2033934
     GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                   protein search, using frame_plus_n2p model
                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                    1017041 seqs, 315518202 residues
                                                                                    US-09-851-410A-6_COPY_5147_7129
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	Oy 1270 GGTATTGCAATCCGCATGACATGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTAT 1329  424 GlylleAlalleProHisAspileAspileAspileAspinSerArgValVallleGlnAspTyr 443  ON 1330 GATAACCAAGAAGAAGAAGAAGACGCCGACCACCATGGGGCGCTTTCTC 1389	444	ValleuargalaasnaspvalleuTrpLeuserLeuThrAlaalaalugfuTyrAspGlnser acmmangacnentnegacngageccagnthangritateattr	488 1.	504	524	544	564	584	604	1970	ValalagluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu	OSWOAD ID QSWOAD PRELIMINARY; PRT; 660 AA. AC QSWOAD, ACKLEMBITED 12. Created)	DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE ORF-2004 (TrEMBLrel. 25, Last annotation update) DE ORF-2005 (TrEMBLrel. 25, Last annotation update)	OC Viruses; ssRNA positive-strand viruses, no DNA stage; OC Hepatitis E-like viruses. OX NCBL TaxID=12461;	-0,0,2,4	Walimbe A.M.; "Phylogenetic analysis of hepatitis E v 1993).";	RL J. Gen. Virol. 80:1691-1/00(1999). DR EMBL; AF124407; AAD45493.1:
SQ SEQUENCE 660 AA; 70903 MW; 1F506BE3CFB3BACE CRC64;	Alignment Scores:  Pred. No.: Score: Score: Score: 99.824 Conservative: Best Local Similarity: 99.824 Tisnatches:	69.09* Indels: 12 Gaps: 	310 ACAGCTGG          104 ThrAlaGl	Qy 370 GATGTCGACTCCCGCGGCGATCTTGCGCCGGCGGTATAACCTATCAACATCTCCCCTT 429	Qy 430 ACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCCTCTTAGTCCGCTT 489	Qy 490 TTACCCCTTCAGGACGGCACCAATACACATATAATGGCCACGGAAGCTTCTAATTATGCC 549	Qy 550 CAGTACCGGGTTGCCCCTGCCACAATCCGTTACCGCCCGC	Qy 610 GGTTACGCCATCTCCATCTCATTCTGGCCACACCACCACCACCACGTCCGTTGAT 669	Qy 670 ATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCTGGCATAGCCTCTGAG 729 Db 224 MetAsnSerIleThrSerThrAspValArgIleLeuValGInProGlyIleAlaSerGlu 243	OY 730 CTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCCGTCGAGACC 789	2y 790 TCTGGGGTGGCTGAGGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCA 849 Db 264 SerClyvalAlaGluGluAlaThrSerClyLeuValMetLeuCysIleHisGlySer 283	Qy 850 CTGGTAAATTCCTATACTAATACACCGTAGCGGTGCCCTGGGGCTGTTGGACTTTGC 909	OY 910 CTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTAT 969	Qy 970 TCCAGCACTGCTCGCCACCGCGTGCGGACGGACTGCCGAGCTCACCACC 1029	QY 1030 ACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAG 1089	Oy 1090 ATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGCTGACACTCTGGCGCCTG 1149	Oy 1150 CCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCA 1209	1210

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TACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGG 1728
          CGTGTGGTTATTCAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCA
                                                          TACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTA
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MEDLINE=S9171571; PubMed=7871758;
MEDLINE=9517571; PubMed=7871758;
Tin S., Pircell R.H., Emerson S.U.;
"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
Virus Genes 9:23-321(1994).
EMBL; L25547; AAA65490.1; -.
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the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=12461;
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InterPro; IPR008975; Viral_cap_coat.
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STRAIN=MOTOCCO;
Carbon G., Meng J.;
Identification of the 5' Capped and 3' Complete Terminal the Hepatitis E virus Isolated From Morocco.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0655061; AAD10627.1; -.
EMBL; AY230202; AAO72992.1; -.
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Hepatitis E-like viruses.
NCBI_TaxID=12461;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein 2 (Structural viral protein).
Hepatitis E virus.
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STRAIN=HEV-Morocco;
STRAIN=99107414; PubMed=9892396; Meng J., Cong M., Dai X., Fillot Khudyakov Y.E.;
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Matches:
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Mismatches:
Indels:
       GO, GO:0005198; F:structural molecule activity; InterPro; IPR004251; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; Pro3014; SP2.
SEQUENCE 660 AA; 70979 MW; DC68116DCD639175
                                                                                                                                                                     COPY_5147_7129 (1-1983) x Q89468
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OGWJZS;
O1-NOY-1999 (TrEMBLrel. 12, Created)
O1-NOY-1999 (TrEMBLrel. 12, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Structural protein 2 (Fragment).
Hepatitis E virus.
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
NCBI_TaxID=12461;
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GO; GO:0005198; F:structural molecule
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pari; PRO:0114; SP2; 1.
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MEDLINE=9221462; FubMed=1589964;
Fry K.B., Tam A.W., Smith M.W., Kim J.P., Luk K.-C., Young L.M.,
Piatak M., Reldman R.A., Yun K.Y., Purdy M.A., McCaustland K.A.,
Bradley D.W., Reyes G.R.,
"Hepatitis B virus (HEV): Strain variation in the nonstructural gene
region encoding consensus motifs for an RNA-dependent RNA polymerase
and an ATP/GTP binding site.";
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MEDLINE-92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Hepatitis E virus (HEV): molecular cloning and sequencing of
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TSATEV S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters Malik I.A., Idbal M., Purcell R.H., "Characterization of a prototype strain of hepatitis E virus. Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
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Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno I
"Hepacitis E virus: cDNA cloning and expression.";
Microbiol. Immunol. 36:67-79(1992).
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Aye T.T., Uchida T., Ma X.Z., Iida F., Shikata T.,
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01-OCT-2003 (TrEMBLrel. 25,
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Virology 185:120-131(1991).
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                       Van Cuyck-Gandre H., Clements N.J., Zhang H.Y., Caudill J.C., Cohen S.G., Coursaget P., Buisson Y., Warren R.L., Longer C.F.; Partial Sequence of HEV Isolates from North Africa and Pakistan: Comparison with Known HEV Sequences."; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
          Caudill J.C.,
fonger C.F.;
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STRAIN=TK15/92;
MEDLINE=99049628; PubMed=9833882;
MHODLINE STRAINGS N., Popek M.J., Longer C.F., Innis B.L.,
"Huppetitis Virus: complete genome sequence and phylogenetic
of a Nepali isolate.";
Virus Res. 57:21-26(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03014; SP2; 1. _ _ SEQUENCE 660 AA; 70798 MW; A04C0185ACC085DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA stage;
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Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no
Hepatitis E-like viruses.
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Q9WLL4;
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01-NOV-1999 (TEMBLrel. 12,
01-OCT-2003 (TEMBLrel. 25,
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              SEQUENCE FROM N.A.
MEDLINE=93348763; bubMed=8346669;
MEDLINE=93348763; bubMed=8346669;
"The sequence of hepatitis E virus isolated directly from a single source during an outbreak in China.";
Virus Res. 28:233-247(193).
EMBL; LO8816; AAAO3191.1; -.
GO; 000198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR004261; SP2.
Pfam; PF03014; SP2; Ural_cap_coat.
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SEQUENCE FROM N.A.
MEDLINE=22072932; PubMed=12076829;
Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
"Reevaluation of a North India isolate of hepatitis E virus based on the full-length genomic sequence obtained following long RT-PCR.";
Virus Res. 86:53-58(2002).
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Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR4554918; AAM66330.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; Viral_cap_coat.
SEQUENCE 659 AA; 70842 MW; ABCC177EBE6012C8 CRC64;
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Viruses; ssRNA positive-strand viruses,
Hepatitis E-like viruses.
VCBI_TaxID=12461;
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von Brunn A., Seebach J., Thyagarajan S.P., Mohanavalli B.,
Proesner G.;
Proesner G.;
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ORF1, ORF2 & ORF3.
Hepatitis B virus.
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InterPro; IPR008975; Viral_cap_coat.
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"Sequence analysis of full length HEV clones derived directly human liver in fulminant hepatitis E.";
III) Rizzetto M., Purcell R.H., Gerin J.L., Verme G (eds.);
VIRAL HEPATITIS AND LIVER DISBASE, pp.313-316,
                                                                                                                                                                                    Viruses; seRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Harrison T.J.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databa
BLBL; X98292; CAR6637.1; -.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
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01-NOV-1996 (TrEMBLrel. 01, Cr
01-JAN-1998 (TrEMBLrel. 05, La
01-OCT-2003 (TrEMBLrel. 25, La
Structural protein.
Hepatitis E virus.
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Best Local Similarity:
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DT 01-0
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OC Viru
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"Phylogenetic analysis of heatitis E virus isolates from Egypt.";
J. Med. Virol. 57:68-74[1999].

BMBL; AF051351; AAC35761.1;
GO; GO:0005199; Festructural molecule activity; IEA.

InterPro; IPR004261; SP2.

InterPro; IPR008975; Viral_cap_coat.
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SEQUENCE 660 AA; 71040 MW; 044FF5EA7C492791 CRC64;
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01-NOV-1998 (TrBMBLrel. 08, Last sequence update)
01-NOV-1998 (TrBMBLrel. 25, Last annotation update)
Structural protein.
Hepatitis E virus.
Viruses; sgrMa positive-strand viruses, no DNA stage;
NGBL TaxID=12461;
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STRAIN=93-EGYPt;
MEDLINE=99105430; PubMed=9890424;
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MEDLINE=99013657; PubMed=9797311;

Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;

Pina S., Jofre J., Emerson S.U., Purcell R.H., Girones R.;

"Characterization of a strain of infectious hepatitis E virus isolated from sewage in a narea where hepatitis E is not endemic.";

Appl. Environ. Microbiol. 64:4485-4488(1998).

EMBL, AF058684; AAC778081.

GO: GO: 0005198; F: Structural molecule activity; IEA.

InterPro; IPR004261; SP2.

InterPro; IPR0084251; Viral_cap_coat.

Pfam; PF03014; SP2; 1.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Structural protein (Fragment).
Hepatitis E virus.
Viruses, SRRNA positive-strand viruses, no DNA stage
Hepatitis E-like viruses.
NCTI TAXID=12461;
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                                                                     STRAIN=94-Egypt;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
MEDLINE=99105430; PubMed=9890424;
Van Cuyck-Gandre H., Longer C.F., Innis B.L.;
"Phylogenetic analysis of hepatitis E virus isolates from Egypt. J. Med. Virol. 57:68-74 (1999).
EMBL; AF051352, AAC35764.1;
GO: GO:0005198; F:Structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR004261; SP2.
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O91856;
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O1-00V-1998 (TrEMBLrel. 08, Le
O1-0CT-2003 (TrEMBLrel. 25, Le
Structural protein.
                                             3.46e-237
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              AA;
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Uchida T.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, D11093; BAA01867.1;
GQ; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03014; SP2; 1. _ _ _ SRQUENCE 660 Aa; 70937 MW; 5412313F1A2EF4A9 CRC64.
                                                                                                                                                                                                                                                                                                           Hepatitis E virus. Junes, viruses, no DNA stage; Hepatitis E-like viruses.
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Mismatches:
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Matches:
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01-NOV-1996 (TrEMBLrel. 01,
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                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=Uigh179;
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STRAIN=BurmaEpi-1-3;
STRAIN=BurmaEpi-1-3;
STRAIN=Bolouse-2024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W.,
Fry K.E., Reyes G.R.;
"Heparitis E virus (HEV): molecular cloning and sequencing of the full-length viral genome.";
Virology 185:120-131(1991).
                                                                                                                                                                                                                                                                                                              Sequence comparison of the capsid region of Hepatitis E viruses isolated from Myanmar and China.";
Microbiol. Immunol. 36:615-621(1992).
EMBL; D1033; BAA01179.1; -.
GO, GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR004261; SP2.
Pfam: PF03014; SP2; 1.
NON TER 28 28 28
SEQÜENCE 248 AA; 26859 MW; 3CB139211E2D045F CRC64:
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BurmaEpi-1-3;
MEDLINE=92396046; PubMed=1387921;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Zhuang H.,
Win K.M.;
                                                                                                   Hepatitis E virus.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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                                                     (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Structural protein (Fragment)
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APPLICANT: Reyes, Gregory R.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Tarbough, Patrice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 38,650,0003 35: COORD
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US - 07 - 876 - 941A - 17

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PCT-US95-13703-15
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TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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11: /cgn2_6/ptodatca/2/iaa/5A_COMB.pep:*

12: /cgn2_6/ptodatca/2/iaa/5B_COMB.pep:*

13: /cgn2_6/ptodatca/2/iaa/6B_COMB.pep:*

41: /cgn2_6/ptodatca/2/iaa/6B_COMB.pep:*

42: /cgn2_6/ptodatca/2/iaa/PCTUS_COMB.pep:*

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44: /cgn2_6/ptodatca/2/iaa/PCTUS_COMB.pep:*

45: /cgn2_6/ptodatca/2/iaa/PcTUS_COMB.pep:*
                                            Compugen Ltd
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US-08-259-148A-19
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US-09-553-427-8
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US-09-553-427-8
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320
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                     CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
                               HisGlySerLeuValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu
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Conservative:
Mismatches:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
CRIGINAL SOURCE:
INDIVIDUAL ISOLATE: F;
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                                                                                          (1-1983) x US-08-259-148A-19 (1-660)
          Conservative:
Mismatches:
Indels:
 Matches:
660.00
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100.00%
                                                                                               US-09-851-410A-6_COPY_5147_7129
          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                  APPLICANT: Krawczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUKKENT APPLICATION DATA:
CUKKENT APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION 1 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 345,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 345,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 2697
FILING DATE: 17-JUN-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUN-1988
ATTOKNEY AGENT INFORMATION:
ANAME: CALLT CAPATION:
                                                                                                                     Sequence 19, Application US/08259148A Patent No. 5741490 GENERAL INFORMATION:
                                                                                                                                                                 APPLICANT: Reyes, Gregory R. APPLICANT: Bradley, Daniel W. APPLICANT: Twu, Jr. Shin APPLICANT: Purdy, Michael A. APPLICANT: Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORF
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MEDIUM TYPE: Floppy disk
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amino acid
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US-08-259-148A-19
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Length:

Alignment Scores: Pred. No.:

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APPLICANT: Tam, Albert W.

APPLICANT: Krawczynski, Krzysztof Z.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                    CALK: 7:300
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-UN-1995
                                                                                                                                            B: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-ARRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
FILING DATE: 13-OCTOBER-1989
FILING APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UINE-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-JUNE-1989
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
        Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 660 amino acids
amino acid
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ADDRESSEE: Dehlinger
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                                                                                                                                                          STREET: 350 Cambr
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity:
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                                          APPLICANT:
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Length:
Matches:
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BURMA, FIGURE
                                                     Indels:
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INDIVIDUAL ISOLATE:
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Query Match:
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4600-0093.38

38,615

US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-08-484-054-19 (1-660)

1 AIGCGCCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGGCGCCA 60

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420 140 480 540 180 009 200 099

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GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT 1140
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                                                       AsnTyralaGlnTyrargValAlaArgAlaThr1leArgTyrargProLeuValProAsn
    ProPheAlaProAspValThrAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla
                                  CGACCACTCGGCTTGGCGTGACCAGGCCCAGCGCCCCGCCGTTGCCTCACGTCGT
                                                                                               AGACCTACCACAGCTGGGGCCGCGCCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCG
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                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAX-1992
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
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Mismatches:
Indels:
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FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0880
INFORMATION POR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LEMATH. CONTRACTERISTICS:
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amino acid
                                       ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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Palo Alto
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Best Local Similarity:
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Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                          NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/279,823
FILING DATE: 25-UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 17-UNW-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                    APPLICATION NUMBER: US 07/505,888 FILING DATE: 05-APR-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/420,921 FILING DATE: 13-OCT-1989
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
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                                                                                                                                  Enterically Transmitted
6120988-B Hepatitis Viral Agent
                                                         1741 ATTICCACTIACACCACTAGCCTGGGTGCTCGCGTCTCCATTICTGCGGTTGCCGTT
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,507
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Patent No. 612098
GENERAL INFORMATION:
APPLICANT: Reves, Gregory R
APPLICANT: Bradley, Daniel W
APPLICANT: Rawczynski, Krzysztof Z
APPLICANT: Tam, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: DNA Sequences of Enter
TITLE OF INVENTION: No. 6120988-A/No. 612;
NUMBER OF SEQUENCES: 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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Matches:
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Mismatches:
Indels:
Gaps:
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  HYPOTHETICAL: NO
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu 660
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APPLICANT: Yarbough, Patrice O
APPLICANT: Yarbough, Patrice O
APPLICANT: Bradley, Daniel W
APPLICANT: Trawcaynski, Krzysztof Z
APPLICANT: Traw, Albert
APPLICANT: Fry, Kirk E
TITLE OF INVENTION: No. 6229005-B Hepatitis Viral Agent
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HIGH PC COMPATION
COMPATION TITLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,275A
FILING DATE: 03-MG-1996
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,078
FILING DATE: 05-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/420,921
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1989
PRIOR APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
ATPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                    STREET: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
STATE: CA
COUNTRY: USA
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REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEFAX: (550) 324-0800
TELEFAX: (550) 324-0960
INFORMATION FOR SEQ ID NO: 8:
                                                                              Sequence 8, Application US/09128275A Patent No. 6229005
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis E Virus (Burma strain)
ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,292
FILING DATE:
PLING APPLICATION PATA:
APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTOMNEY/AGENT INFORMATION:
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Conservative:
Mismatches:
                              Desjardins, M.D.
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                                                                                                                                                                                                                                                                                        NAME: Brookes, Allan A
REGISTRATION NUMBER: 35,373
REFERENCE/DOCKET NUMBER: G32P5
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415)369-9500
TELEPAX: (415)369-0709
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  NUMBER OF SEQUENCES: 24
CORRESPONDENCES:
CARDRESSEE: Cathleen M. Desj
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                          : 660 amino acids
amino acid
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Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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                                                      Redwood City
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                           ADDRESSEE:
STREET: 505
CITY: Redwc
STATE: CA
COUNTRY: US
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-477-292-13
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GlyGlyLeuProThrGluLeuIleSerSerAlaGlyGlnLeuPheTyrSerArgPro
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                                            GTCGGTGAGATCGGCCGCGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTT
                                                                                                 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC
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APPLICANT: Fuerst, Thomas
APPLICANT: McAtee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Zhang, Yifan
IIILE OF INVENTION: Hepatitis E Virus Antigens and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-477-292-13
; Sequence 13, Application US/08477292
; Patent No. 6291641
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361 CCAGTGCCTGATGTCGACGCCCCGCGGCCATCTTGCCCCGGCAGTATAACCTATCAACA 420 [	1 TCTCCCCTTACCTCTCCGCGCACCACACCTGCTTTTATGCCGCCCCTTT 48		541 AATTATGCCCAGTACCGGGTTGCCCGTGCCAATCCGTTACCGCCCGC	601 GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCGGACG 660 	661 TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720 		781 GTCGAGACCTCTGGGGTGGGTGGAGGGGAGGCTACCTCTGGTCTTGTTATGCTTTAGCATA 840 	841 CATGGCTCACTCGTAAATTCCTATACTAATACCATACCGTATACCGGGCTGCCTCGGGCTGTTG 900 	901 GACTITGCCCTTGAGCTTGGCAACCTTACCCCGGTAACACCAATACGCGGGTC 960 	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCTTCGTCGCGGGCGG	1021 CTCACCACCACGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080 	1081 GTGGGTGAGATCGGCGGGGATAGCCCTCACCGTGTTCAACCTTGCTGACACTCTGCTT 1140	1141 GGCGGCCTGCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCC 1200 	1201 GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG 1260 	1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320 	1321 CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC 1380	1381 CCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT	1441 GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTG 1500
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 SerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMetAlaThrGluAlaSer
                                    241 AlaSerGluLeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer
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                        GCTGTCGCCGGTTACGCCATCTCCATTTCTGGCCACAGACCACCACCACCGACG
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660
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Matches:
Conservative:
Mismatches:
Indels:
APPLICATION NUMBER: US 07/505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/367,486
FILING DATE: 16-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/336,672
FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/208,997
FILING DATE: 11-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles R.
REGISTRATION NUMBER: 4600-0183.22
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 4600-0183.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
INFORMATION FOR SEG 1D NO: 8:
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660.00
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LENGTH: 660 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-553-427-8
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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ATAAT 168        YrAsn 560 YrAsn 560        alala 580 CCGTT 180        laval 600        rgala 620	Db 621 HisThTFATURATION CARACTEGE CCCCCTTTGGGGGGGGGGGGGGGGGGGGGGGGGG	Sequence 50, Application US/09462606  Batent No. 6432408  GENERAL INFORMATION:  APPLICANT: MENG, XIANG-JIN  APPLICANT: Emerson, Suzanne U.  APPLICANT: Purcell, Robert H.  TITLE OF INVENTION A SWINE HEPATITIS E VIRUS AND USES THEREOF  FILE REPERBUCE: 20264267US1  CURRENT APPLICATION NUMBER: US/09/462,606  CURRENT APPLICATION NUMBER: US/09/462,606	FRICK PILING DATE: 1997-07-18  PRIOR PILING DATE: 1997-07-18  PRIOR APPLICATION NUMBER: PCT/US98/14665  PRIOR PILING DATE: 1998-07-17  NUMBER OF SEQ ID NOS: 65  SOFTWARE: Patentin Ver. 2.1  SEQ ID NO 50  LENGTH: 660  TYPE: PRT  ORGANISM: Hepatitis E virus	Alignment Scores: Pred. No.: Score: Score: Score: Best Local Similarity: 100.00\$ Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Mismatches: 0 Indels: 0 DB: 4 Gaps: 0 US-09-851-410A-6 COPY 5147 7129 (1-1983) x US-09-462-606-50 (1-660)	Oy 1 ATGGGCCTCGGCCTATTTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGGCCA 60

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301 AGACCTACCACAGCTGGGGCGGCGCGCTAACCGCGGTCGCTCCGGCCCATGACACCCCG 360
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                        NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 82,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRLI-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCYDER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 367,886
FILING DATE: 11-APRLI-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRLI-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRLI-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
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Best Local Similarity:
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                                            441 GlnAspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArg 460
                                                                                                                 561 TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla 580
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                       CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
                                                                                                                                                                                          481 AspGlnSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu
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Patent No. 6455492

GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Purdy, Daniel W.
APPLICANT: Purdy, Albert W.
APPLICANT: Tau, Albert W.
APPLICANT: Tau, Albert W.
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APPLICANT: Tau Albert W.
APPLICANT: Correspondences: 22
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
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350 Cambridge Avenue, Suite 250
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-07-870-985A-19
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21 ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 21 TCTCCCCTTACCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCTCTT	erProL GTCCGC        erProL	AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCGGCTGGTCCCCAAT	601 GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCGCGGG 660 	661 TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720 	721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780 	781 GTCGAGACCTCTGGGGTGGCTGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATA 840		901 GACTTIGCCCTIGAGCTIGGGAGCTTTGGCAACCTTACCCCCGGTAACACCAAIACGGGGGTC 960 	961 TCCCGTTATTCCAGCACTGCTCGCCACCGCCGTCGTCGCGGTGCGGACGGA	1021 CTCACCACCACGGCTACCCGGTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080 	1081 GTCGGTGAGATCGGCCGCGGATAGCCCTCACCCTGTTCAACCTTGCTGCTCACCTCTGCTT 1140 	1141 GGCGCCTGCCGACAGAATTGATTTCGTCGGCTGGTCGCCGGTCTTCTACTCCCGTCCC 1200 	1201 GTTGTCTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG 1260 	1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 1320 	1321 CAGGATTATGATAACCAACAAGAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC 1380 	1381 CCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT	1441 GACCAGTCCACTTAIGGCTCTTCGACTGGCCCAGTTTAIGTTTCTGACTCTGTGACCTTG 1500 

901 GACTITGCCCTTGAGCTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC 960	1081 GTCGGTGAGATCGGCGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGGTT 1140	GLGGCCACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1261 CAGGATAAGGGTATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTGTTT 1320	CCTTTCTGTCCTTCGAGCTAATGATGTGCTTTGGCTCTCTCT	rGlySerSerThrGlyProvalTyrvalSerA. CGGCGCGAGGCCGTTGCCCGGTCGCTCGATTV 	1561 CTTGACGGTCGCCCTCTCCACCATCAGAGACTACTCGAAGACCTTCTTGTCCTGCCG 1620	1681 TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT 1740	IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal 60 TTAGCCCCCCACTCTGGGCTAGCATTGCTTGAGGATACCTTGGACTACCTGGCCGGCC	1861 CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTTGAGGGCTGCGCTTTC 1920	641 GlnS 13
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INDIVIDUAL ISOLATE: ORF-2 -US95-13703-13 gnment Scores: 0. No.: 660.00 Matches: 660 cent Similarity: 100.00% Conservative: 0 t Local Similarity: 100.00% Mismatches: 0 ry Match: 560.00 Matches: 660 cent Similarity: 100.00% Conservative: 0 t Local Similarity: 100.00% Mismatches: 0 sy Match: 100.00% Gaps: 0	-09-851-410A-6_COFT_514/_/129 (1-1985) X PCT-0595-13/03-13 (1-660)  1 ATGCGCCTCGGCCTATTTGTTGCTGCTCCTCATGTTTTTGCCTATGCTGCCGCGCCA 60	61 CCGCCCGGTCAGCCGCCCGTCGTGGGCGCGCAGCGGCGGTTCCGGCGGTGGT 120 [	CCCTTCGCCCCCGATGTCACCGCTGCGGCCGGGGCTGGACCTCGTGTTCGCCAACCCGCCCCGCCGCGCTGGACTTCGCCAACCCGCCGCCGCGCGGGGCTGGAAAAAAAA	ASPICOCUCINES SENTIAL IN PAIGRS DE LIMITACIDAL EN LA BARCETACACACCACCACACCACACACACACACACACACACAC		AGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAAGCTTCT	snfyrAladinfyrArgValAlaArgAlafhrileArgfyrArgProLeuValP CTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCACCCCCCCC	TCCGTTGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGCCATA 7 [[		

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ACAACTAAAGCCGGGTACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTC 1713
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TGGCCACAGACCACCACCCCGACGTCCGTTGATATGAATTCAATAACCTCGACGGAT
                                                               GTTCGTATTTTAGTCCAGCCCCGGCATAGCCTCTGAGCTTGTGATCCCCAAGTGAGCGCCTA
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                                                            APPLICANT: Puezet, Thomas R.
APPLICANT: Puezet, Thomas R.
APPLICANT: Azhough, Patrick
APPLICANT: Azhough, Patrice O.
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEM
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 324-080
TELEPAX: (415) 324-080
TELEPAX: (415) 324-080
TELEPAX: (415) 324-080
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Matches:
Conservative:
Mismatches:
Indels:
    US-08-542-634-15
; Sequence 15, Application US/08542634
; Patent No. 6214970
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TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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549.00
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                                                GENERAL INFORMATION:
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Best Local Similarity:
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Length: Matches: Conservative: Mismatches:

Indels:

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CGTCGCGGTGCCGACGGACTGCCGAGCTCACCACGGCTGCTACCCGCTTTATGAAG 1053
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                                                Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15. Application US/08477292
Patent No. 6291641
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas
APPLICANT: Mackee, Patrick
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/08/477,292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Cathleen M. Desjardins, M.D. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                      ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
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r62kDa, FIGURE 4
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APPLICATION NUMBER: US/08/327,952
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Brookes, Allan A REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: G32F!
TELECHONIC (A15)369-9500
TELEPHONE: (415)369-9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELBFAX: (415)368-0709
INFORMATION FOR SEQ ID NO: 15:
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amino acid
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LENGTH: 549 amino aci
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Alignment Scores

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                                                                                                                                                                                                               strain)
                                                                                                                                                                                                                                                                                   Hepatitis E virus (Burma
r62kDa, FIGURE 4
                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 549 anino acids
TYPE: amino acids
TYPE: amino acids
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Matches:
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83.18%
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                          single
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PCT-US95-13703-15
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ArgSerLeuAspTrpThrLysValThrLeuAspGlyArgProLeuSerThrlleGlnGln
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILICATION NUMBER: PCT/US95/13703
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1954 ATGAAGGIGGGTAAAACTCGGGAGTTG 1980
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STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
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Search completed: August 16, 2004, 13:59:39 Job time : 57.0151 secs

Hank Sheet

protein search,

on:

Ygapop Fgapop Delop Xgapop OLIGO

Word size:

Searched:

Title: Perfect score:

Sequence:

Scoring table:

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Sequence 11, Appl
Sequence 21, Appl
Sequence 34, Appl
Sequence 92, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 22, Appl
Sequence 175, Appl
Sequence 175, Appl
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Sequence 25, Appl
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Sequence 17, Appl
Sequence 1, Appli
Sequence 17, Appl
Sequence 13, Appl
Sequence 8, Appli
Sequence 19, Appl
Sequence 15, Appl
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Sequence 199, 1
Sequence 200, 1
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Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGENS AND USES THEREFOR
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                         4 US-09-769-066-17

4 US-10-165-868-15

2 US-10-381-770-12

2 US-10-381-770-12

2 US-10-381-770-13

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US-10-239-090A-55

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US-09-468-147-175
US-09-468-147-176
US-10-319-745-175
US-09-468-147-199
US-10-319-745-199
US-10-319-745-200
US-09-468-147-206
US-09-468-147-206
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US-10-381-770-1
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ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
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APPLICANT: Fuerst, Thomas R.
  CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
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-Q=/cgn2 1/USFTO_spool p/US09851410/runat_16082004_125719_9771/app_query.fasta_1.4238
-D=-Cgn2 1/USFTO_spool p/US09851410/runat_16082004_125719_9771/app_query.fasta_1.4238
-D=-UGD=UGD=UGD=V=DEV=DEV=DEV=Z=RAT=1 -END=-1 -MATRIX=0ligo
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-MAXLEN=2000000000 -USER=US09851410 @CGN 1 1_27 @runat_16082004_125719_9771
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                     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                          using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                        US-09-851-410A-6 COPY 5147 7129
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60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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Maximum DB seq length: 2000000000
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Query Match Length DB

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                          NAME: FADIAI, GATY R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
WATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       Virus
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1
                                                                                                                                                                                     STRANDEDNESS: Hepatitis
                                                                                                                                                                LENGTH: 660 amino acids TYPE: amino acid
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Query Match:
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Pred. No.:
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Matches:
Conservative:
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO
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Best Local Similarity:
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No. US20030124510A1-A/No. US20030124510H-B Hepatitis Viral
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 LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn
                                               ATTICCACITACACCACTAGCCTGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
                                                                                                              CATACTTTTGATGATTTCTGCCCCAGAGTGCCGCCCCCTTGGCCTTCAGGGCTGCGCTTTC
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                              TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
                                                                                                                                                         TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SEARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0860
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,410
FILING DATE: 0.7-May-2001

PRIOR APPLICATION NUMBER: US/09/851,410

APPLICATION NUMBER: 09/128,275
FILING DATE: 0.5-APR-1991

APPLICATION NUMBER: US 07/505,888
FILING DATE: 0.5-APR-1990

APPLICATION NUMBER: US 07/505,888
FILING DATE: 0.5-APR-1990

APPLICATION NUMBER: US 07/505,888
FILING DATE: 13-0CT-1989

APPLICATION NUMBER: US 07/367,486
FILING DATE: 13-0CT-1989

APPLICATION NUMBER: US 07/367,486
FILING DATE: 14-0V1-1989
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FILING DATE: 11-APR-1989
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FILING DATE: 17-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reyes, Gregory R
Yarbough, Patrice O
Braddey, Daniel W
Krawczynski, Krzysztof
Tam, Albert
Fry, Kirk E
                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09851410 Publication No. US20030124510A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94306
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEOUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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COUNTRY: U
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                                                                                            1741
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CAGICIACIGICGCICAGCIIICAGCGCCTIAAGAIGAAGGIGGGIAAAACICGGGAGIIG 1980
                              641 GlnSerThrValAlaGluLeuGlnArgLeuLySMetLySValGlyLySThrArgGluLeu 660
                                                                                                                                                                                                                   Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APPLI-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APPLI-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                    ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Unn-2002
CLASSIFICATION: <Unknown>
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NO: 19:
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APPLICATION NUMBER: 03.36,672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 367,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 324-0880
                                                                                     US-10-165-868-19; Sequence 19, Application US/10165868; Publication No. US20030143241A1
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SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                            Purdy, Michael A.
Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 660 amino acids
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R
Bradley, Daniel
Twu, Jr-Shin
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100.00%
100.00%
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                  STATE: CA
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Best Local Similarity:
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                                                                                                                                                  TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCCGAG 1020
                                                                                                                                                                                                             CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT 1080
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                                               LeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheValLeuPro
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                              CATGGCTCACTCGTAAATTCCTATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTG
                                                                                        GACTITIGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACACAATACGCGGGTC
                                                                                                         AspPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgVal
                                                                                                                                                                     SerArgTyrSerSerThrAlaArgHisArgLeuArgArgGlyAlaAspGlyThrAlaGlu
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Query Match:         100.00%         Indels:         0           DB:         14         Gaps:         0           US-09-851-410A-6_COPY_5147_7129         (1-1983) x US-10-165-868-19         (1-660)           QY         1 ATGGGCCTGGGCTATTTTGTTGCTGCTCCTCATGTTTTGCTATGCTGCGGGGCA         60           Db         1 MetArgProArgPro1leLeuLeuLeuLeuLeuLeuLeuMetPheLeuProMetLeuProAlaPro         20           QY         61 CGGCCGGTCTGGGCGGCGTGGGGGGGGGGGGGGGGGGG	TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	61 ProPheAlaProAspValThrAlaAlaAlaAlyAlaGlyProArgValArgGlnProAla 80 241 CGACCACTCGGCTTGGCGTGACCAGCCCCAGCGCCCCGCTTGCCTCACGTCGT 300 241 CGACCACTCGGCTTGGCGTGACCAGCCCCAGCGCCCCGTTGCCTCACGTCGT 300 81 ArgProLeuGlySerAlaTrpArgAspGlnAlaGlnArgProAlaValAlaSerArgArg 100 301 AGACCTACCACAGGGCCGGCCGGCTGCCGCCGCTCGCCCCGCCCCAGACCCGG 360 111111111111111111111111111111111111	101 ArgProThrThrAlaGlyAlaAlaProLeuThrAlaValAlaProAlaHisAspThrPro 120 361 CCAGTGCCTGAUGTCGACGCGCGCGCGCATCTTGCGCCGGCAGTATAACCTATCAACA 420		161 SerProLeuLeuProLeuGlnAspGlyThrAsnThrHisIleMeCAlaThrGluAlaSer 180 541 AATTATGCCGGTACCGGGTTGCCGGTGCCAAATCCGTTACCGCCGGTGGTCCCCAAT 600 [	201 AlaValGlyGlyTyrAlaileSerileSerPhefTpProGliff	721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCCTCC 780		Oy 901 GACTTTGCCCTTGAGTTTCGCAACCTTACCCCGGTAACACCAATACGCGGGTC 960

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   TrpProGlnThrThrThrThrProThrSerValAspMetAsnSerIleThrSerThrAsp 120
                                                   ValArgileLeuValGlnProGlyIleAlaSerGluLeuValIleProSerGluArgLeu
                                                                                                               HisTyrArgAsnGlnGlyTrpArgSerValGluThrSerGlyValAlagluGluGluAla
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                                                                                                                                                                           ThrSerGlyLeuValMetLeuCysIleHisGlySerLeuValAsnSerTyrThrAsnThr
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                                 GTTCGTATTTTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTA
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                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION: AUKNOWN>
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Matches:
Conservative:
Mismatches:
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TITLE OF INVENTION: HEPATITIS E VIRUS A
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/542,634
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,875
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MOLECULE TYPE: protein

HYPOTHETICAL: NO

CHIGINAL SURCE:

SEQUENCE DESCRIPTION: SEQ ID

US-09-769-066-15
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SEQUENCE CHARACTERISTICS:
                                                                                                       COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
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                                                              1893
                                                                                                                CCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAG 1953
                                                                                                                                         540
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                         ProValSerIleSerAlaValAlaValLeuAlaProHisSerAlaLeuAlaLeuGlu
                                                                           AspThrLeuAspTyrProAlaArgAlaHisThrPheAspAspPheCysProGluCysArg
                                                                                                                            ProAlaArgProLeuGlySerAlaTrpArgAspGlnAlaGlnArgProAlaValAlaSer
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            CCCGTCTCCATTTCTGCGGTTGCCGTTTTTAGCCCCCCCACTCTGCGCTAGCATTGCTTGAG
                                                              GATACCTTGGACTACCCTGCCCCGCGCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC
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                                                                                                                                                                                                                                        Sequence 1, Application US/10257044
Publication No. US20030220475A1
Publication No. US20030220475A1
GABERAL INFORMATION:
APPLICANT: The Government of the United States of America, as APPLICANT: Heman Services, Centers for Disease Control and Prevention APPLICANT: Human Services, Centers for Disease Control and Prevention APPLICANT: YURI B. KHUNYAKOV
APPLICANT: JIHONG MENG
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NEUTRALIZING IMMUNOGENIC HEV POLYPEPTIDES (HEV)
FILE REFERENCE: 14114.0340U2
CURRENT APPLICATION NUMBER: US/10/257,044
CURRENT FILING DATE: 2001-00-4
PRIOR PELING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
LENGTH: 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-10-257-044-1 (1-660)
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                   ATGAAGGTGGGTAAAACTCGGGAGTTG 1980
                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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541.00
99.84%
99.84%
81.97%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                              1894
                                   481
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                                                                                                                                      E virus (Burma strain)
                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
               REFERENCE/DOCKET NUMBER: 4600-0293.30
                                                                                                                                                                                                                                                                                                                                                   Indels:
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
STRANDEDNESS: Hepatitis E virus
TOPOLOGY: linear
                                                                                                                                                                                                                             25
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REGISTRATION NUMBER: 33,875
                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                    540.00
100.00%
100.00%
81.82%
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Query Match:
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                                                                                           TyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArg
                                                                                                                                                                                                                                                                                                                     GTCGCTATTTCCACTTACACCACTAGCCTGGCTGCTGGTCCCGTCTCTCTGCGGTT
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                                                                           ACCTTGGTTAATGTTGCGACCGGCGCGCAGGCCGTTGCCCCGGTCGCTCGATTGGACCAAG
                                                                                                                                       GTCACACTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTC
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                               ValThrLeuAspGlyArgProLeuSerThrIleGlnGlnTyrSerLysThrPhePheVal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/542,634
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Burma
 NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPONE: (415) 324-0860
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/769,066
FILING DATE: 24.Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Pablan, Gary R.
REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus
5 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r62kDa, 56.5
                                                                                                                   ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 525 amino acids
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                         USA
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Best Local Similarity:
Query Match:
DB:
                                                                                      STATE: CA
                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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GGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCAATGGCGAGCCGACTGTTAAG
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                                                      GACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATCGGCCGCGGGGATAGCCCTCACC
                                                                                                                           CTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCGACAGAATTGATTTCGTCGGCT
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MCAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/09769066 Patent No. US20020107360A1 GENERAL INFORMATION:
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US-09-769-066-27
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                                                                                   GATACCTTGGACTACCCTGCCCGCGCCCCATACTTTTGATGATTTCTGCCCAGAGTGCCGC
                                                                                                                                                                                                                                                                        APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr.-Shin
Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
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APPLICATION DATA:
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 22, 335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 50, 888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420, 921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 327, 486
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 336, 672
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 336, 672
FILING DATE: 11-APRIL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: C2, BURMA, E SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 466
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                            Sequence 17, Application US/10165868 Publication No. US20030143241A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 436 amino acids
TYPE: amino acid
                                                                                                                              1894 CCCCTTGGCCTTCAG 1908
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         521 ProLeuGlyLeuGln 525
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
COUNTRY: USA
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US-10-165-868-17
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US-10-	165-868-17	
Alignme Pred. N Score: Percent Best Lo Query M	I. No.: 0 Length: 436 I. No.: 436.00 Matches: 436 iei: 100.00\$ Conservative: 0 i. Local Similarity: 100.00\$ Mismatches: 0 y Match: 66.06\$ Indels: 0 14 Gaps: 0	1633 CTCTTTCTGGGAGGCAGGCACACTAAAGCCGGGTACCCTTATAATTATAACACCACT 16 1633 CTCTTTCTGGGAGGCAGGCACACTAAAGCCGGGTACCCTTATAATTATAACACCACT 16 121 LeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThr 34 1693 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCTATTTCCACTTAC 17 1694 GCTAGCGACCAACTGCTTGTCGAGAATGCCGCGGGCACCGGGTCGCTATTTCCACTTAC 17 110
-60-SD	851-410A-6_COPY_5147_7129 (1-1983) x US-10-165-868-17 (1-436)	
<i>≿</i> 8	673 AATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCGGCATAGCCTCTGAGCTT 732	361 ThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaValLeuAlaProHis
yy qo	733 GTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGGGCTCCGTCGAGACCTCT 792 	381 SerAlaLeulleugluAspThrLeuAspTyrProAlaArgAlaHisThrPheAsp
S Q	793 GGGGTGGCTGAGGAGGCTACCTCTGGTCTTTGCTTATGCTTACATGGCTCACTC 852	GATTTCTGCCCAGAGTGCCGCCCTTGGCCTTCAGGCTTTCCAGT 
yo da	853 GTAAATTCCTATACTAACACCCTATACCGGGGCTGCCCTCGGGCTGTTGGACTTTGCCCTT 912	<u>ہ</u> ہ
oy D	913 GAGCTTGAGTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCC 972 	RESULT 9 US-10-31-770-1 ; Sequence 1, Application US/10381770 ; Publication No. US20040052813A1
oy du	973 AGCACTGCTGCCACCGCTTCGTCGCGGTGCGGACGGGACTGCCGAGCTCACCACCACG 1032 	J
oy qu	1033 GCTGCTACCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGTGTCGGTGAGATC 1092 	
ys da	1093 GGCGGGGGGATAGCCCTCACCCTGTTCAACCTTGCTGACACTCTGCTTGGCGGCCTGCCG 1152 	SOCIWARE: FACENTIN VERSION SSO ID NO 1 LENGTH: 660 TYPE: PRT
λ 6	1153 ACAGAATTGATTTCGTCGGCTGGTGCTCTTCTACTCCCGTCCCGTTGTCTCAGCC 1212 	Sm: nepartus B vitus 770-1 Scores:
g ç	1213 AATGGCGAGCGACTGTTAAGTTGTATACATCTGTAGAAATGCTCAGCAGGATAAGGGT 1272 	0 408.00 1arity: 99.80% imilarity: 99.80%
ò a	1273 ATTGCAATCCCGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATTCAGGATTATGAT 1332 	indel8: Gaps: (1-1983) x US-10-381-7
<b>7</b> 0, dd	1333 AACCAACAAGAACAAGATGGGCGAGGCCTTCTCCCAGCCCCATGGGCCCTTTCTCTGTC 1392	Oy         289         GCCTCACGTCGTAGCTACCACAGCTGGGGCCGCGCGCTCGGGTCGGTC
yy da	1393 CTTCGAGCTAATGATGTGCTTTTGGCTCTCTCACCGCTGCCGGTTATGACCAGTCCACT 1452 	QY         349 CATGACACCCGCGAGTGCCTGATGTCGACTCCCGGGGCGCCATCTTGCGCCGCAGATAT 408           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
λ Q	1453 TATGGCTCTTCGACTGGCCCAGTTTATGTTTCTGACTCTGTGACCTTGGTTAATGTTGCG 1512 	Qy         409         AACCTATCAACATCTCCCCTTACCGCTCTCGGGCCACGGGACTAACCTGGTTCTTAA         468           137         48         48         48           137         AsnLeuSerThrSerProLeuThrSerSerValAlaThrGlyThrAsnLeuValLeuTyr         156
λ Q	1513 ACCGGCGCGCAGCCGTTGCCCGGTCGATTGGACCAAGGTCACACTTGACGGTCGC 1572 	OY 469 GCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGCCACCATATAGTGGCC 528
ò	1573 CCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAG 1632	Oy 529 ACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCG 588

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TACCCTTATAATTATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGG 1728
    537 PheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGly 556
                                                                                                           HisArgValAlaileSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSer
                                                TyrProTyrAsnTyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGly
                                                                                          CACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCT
                                                                                                                                                                                                                                                                                  APPLICANT: Fuerst, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
Mismatches:
Indels:
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REGISTRATION UNBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                     GCGGTTGCCGTTTTAGCCCCCCACTCT 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/542,634
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NO: 17:
                                                                                                                                                                    597 AlaValAlaValLeuAlaProHisSer
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TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                          Sequence 17, Application US/09769066 Patent No. US20020107360A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID I
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STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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Best Local Similarity:
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                                                                                                                            ThrThrProThrSerValAspMetAsnSerIleThrSerThrAspValArgIleLeuVal
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Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TILE OF INVENTION: Hepatitis B Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       COMPUTER LEADANG disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION: cUnknown>
PRIOR APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 65,888
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 65,888
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 420,921
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0860
                                                                                                                                                                                 ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
Twu, Jr-Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 327 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                       ZIP: 94306
COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                          STATE: CA
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Best Local Similarity:
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                   GGTGCGGACGGGACTGCCGAGGTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTC 1059
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US-10-165-868-15
; Sequence 15, Application US/10165868
; Publication No. US20030143241A1
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                                                                                           327
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE;
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-165-868-15
                                                                                           2.51e-293
327.00
100.00%
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Sequence 12, Application US/10381770

Publication No. US20040052813A1

GRNERAL INFORMATION:
APPLICANT: YANG SHENG TANG company, Ltd.
TITLE OF INVENTION: THE POLYEEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPO
TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REPERENCE: IEC010037PCT
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Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                              5.37e-185
210.00
100.00%
100.00%
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                                                                                             virus
                                                                                             , ORGANISM: hepatitis
US-10-381-770-2
                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                     gnment Scores:
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                                                                   LENGTH: 214
TYPE: PRT
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Publication No. US20040052813A1

GENERAL INFORMATION:

APPLICANT: YANG SHENG TANG company, Ltd.

TITLE OF INVENTION: THE POLYEPPTIDE FRACHENT OF HEPATISIS B VIRUS, THE VACCINE COMPOS

TITLE OF INVENTION: COMPRISING SAID FRACHENTS AND THE DIAGNOSTIC KITS

FILE REPERENCE: IEC010037PCT
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APPLICANT: YANG SHENG TANG COMPANY, Ltd.

TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOSITITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REFERENCE: IECO10037PCT
CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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Mismatches:
Indels:
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Matches:
   CURRENT APPLICATION NUMBER: US/10/381,770 CURRENT FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 SEQ ID NO 4
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// Publication No. US20040052813A1
// GENERAL INFORMATION:
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Publication No. US20040052813A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THE POLYPEPTIDE FRAGMENT OF HEPATISIS E VIRUS, THE VACCINE COMPOS
TITLE OF INVENTION: COMPRISING SAID FRAGMENTS AND THE DIAGNOSTIC KITS
FILE REFERENCE: IEC010037PCT
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CURRENT APPLICATION NUMBER: US/10/381,770 CURRENT FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 12 LENGTH: 232
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; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: hepatitis E virus
US-10-381-770-3
                                                                    Percent Similarity:
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Sequence 16, App
Sequence 176, Ap
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Sequence 12, App
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Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGENS AND USES THEREFOR
CORRESPONDENCES: 3.1
CORRESPONDENCE ADDRESS:
                                                                           Sequence 14, 7
Sequence 20,
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Sequence 175
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                                                               Sequence 1,
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                Sequence
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                        US-09-769-066-14

US-10-165-868-20

US-10-239-090A-57

US-10-239-090A-53

US-10-239-090A-53

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US-09-468-147-92

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US-09-769-066-25

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US-10-319-745-207

US-10-319-745-207

US-10-319-745-199

US-09-468-147-200

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STREET: 350 Cambridge Ave., Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
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 COUNTRY: USA
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   Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cgn2_1/USPTO_spool_p/US09851410/runat_16082004_125455_8610/app_query.fasta_1.4238
-Q=/Cgn2_1/USPTO_spool_p/US09851410/runat_16082004_125455_8610/app_query.fasta_1.4238
-DB=Published Applications AA -QFMT=fastan -SUFFTX=n2p.rapb -MINNATCH=0.1
-LOOPCIL=0 -LOÖPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRX=blosum62
-TRANS=human40.cdi -L15T=45 -DOCALIGN=200 -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HBARSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US09851410 @CGN 1 1 27 @runat 16082004 125455_8610
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-LONGLOG -DEV TIMBOUT=12 -WARN TIMBOUT=30 -THRRADS=1 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                Compugen Ltd.
                                                                            - protein search, using frame_plus_n2p model
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                            August 16, 2004, 13:00:26
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                   Virus (Burma
                                                                                    NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
WATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
 APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: <Unknown>
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/542,634
FILING DATE: <Unknown>
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S
                                                                                                                                                                                                                  STRANDEDNESS: Hepatitis E ORF-2
                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID 1
                                                                                                                                                                                        LENGTH: 660 amino acids TYPE: amino acid
                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                            5.91e-243
3408.00
100.00$
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                       US-09-769-066-13
                                                                                                                                                                  INFORMATION
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                                                                                                                                                                         660
660
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                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                             Gaps:
                                                                                                        ..
8
                                             TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-851-410-8
                                    LENGTH: 660 amino acids
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       5.91e-243
3408.00
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100.00%
93.40%
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Best Local Similarity:
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                                                                                                                                                                         Pred. No.:
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No. US20030124510A1-A/No. US20030124510A1-B Hepatitis Viral
                                                                                                      1800
                                                                                                                                                                         1860
                                  TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT 1740
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                                                                                                                                                                                                                                                                                                                                  LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn
                                                       TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla
                                                                                                      ATTICCACTIACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTICTGCGGTTGCCGTT
                                                                                                                        581 IleSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVal
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COMPUTER: 1BM PC compatible

COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/851,410

FILING DATE: 07-May-2001

APPLICATION NUMBER: 09/128,275

FILING DATE: CURKNOWN:

APPLICATION NUMBER: US 07/681,078

FILING DATE: 05-APR-1991

APPLICATION NUMBER: US 07/505,888

FILING DATE: 05-APR-1990

APPLICATION NUMBER: US 07/505,486

FILING DATE: 13-OCT-1989

APPLICATION NUMBER: US 07/336,672

FILING DATE: 11-JUN-1989

APPLICATION NUMBER: US 07/336,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4600-0183.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reyes, Gregory R
Yarbough, Patrice O
Bradley, Daniel W
Krawczynski, Krzysztof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09851410 Publication No. US20030124510A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tam, Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kirk E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-851-410-8
                                  1681
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CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGATGAAGGTGGGGTAAAACTCGGGGAGTTG 1980
                                 641 GlnSerThrValAlaGluLeuGlnArgLeuLysMetLysValGlyLysThrArgGluLeu
                                                                                                                                                                                                               Purdy, Michael A.
Tam, Albert W.
Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
NUMBER OF SECURICES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #1.25
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660
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COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version f
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BURMA, FIGURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0093.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/07/870,985A
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRLL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRLL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APPLL-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APPLL-1989
APPLICATION NUMBER: US 397,486
FILING DATE: 11-APPLL-1989
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE: ORF 2, B SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
COUNTY: USA
ZIP: 942A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                              US-10-165-868-19
; Sequence 19, Application US/10165868
; Publication No. US20030143241A1
; GENERAL INFORMATION:
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LENGTH: 660 amino acids
TYPE: amino acid
                                                                                                                                                               APPLICANT: Reyes, Gregory R
Bradley, Daniel
Twu, Jr-Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 19:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity:
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Pred. No.:
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Query Match:         93.40*         Indels:         0           DB:         14         Gaps:         0           US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-10-165-868-19 (1-660)         (1-660)           QY           ATGCGCCCTCGGCCTATTTTGTTGCTTTTTTTTTTTTTT	181 CCCTTCGCCCCGATGTCACCGCTGCGGCCGGGACCTCGTGTTCGCCAACCCGCC 240  61 ProPheAlaProAspValThiAlaAlaAlaGlyAlaGlyProArgValArgGlnProAla 80  241 CGACCACTGGCTCGCTTGGCGTGACCAGGCCCGGCGTTGCCTCAGTCGT 300  1	AGTCCGCTTTACCCCTTCAGGACGCACAATACCATATAATGGCCACGGAAGCTTCT	241 Alasertulbuvallieprosergluargleuhisiyrargasndinglyfrpargser 260 781 GTCGAGACCTCTGGGGTGGCTGAGAGAGGCTACCTCTGGTCTTATGCTTATGCATA 840 261 ValGluth/SerGlyValAlaGluGludlaThr/SerGlyLeuValMetLeuCysile 280 841 CATGGCTCACTCGTAAATTCCTAACTACTAATACACCTTATGCGTGTG 300 841 CATGGCTCACTCGTAAATTCTAAATACACCTATACGGGGCCCCTCGGGTGTTG 300 841 CATGGCTCACTCGTAAATTCGTAATACACCCTATACGGGGCCCCTCGGGGTGTTG 300 841 CATGGCTCACTCGTAAATTCGTAATACACCCTATACGGGGGTGTTG 300 841 CATGGCCTTGGGGTTGGGTTTCGCAACTTACCCCTAATACGGGGGTC 300 851 HisGlySerLeuValAanSerTyrThr/AsnThr/AsnThr/AsnThr/ArgVal 320 961 GACTTTGCCGTTGGTCGCCACCGCCTCGTCGCGGGGGGGG

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Matches:
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 CURRENT APPLICATION NUMBER: US/10/381,770
CURRENT FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 660
TYPE: PRT
CORGANISM: hepatitis E virus
US-10-381-770-1
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qq	361	aldıydlullediyArgdiyileAlaLeuThrLeuPheAsnLeuAlaAspThı
ογ	1141	
Dp	381	lydlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgPr
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QQ	401	lValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln 42
δ	1261	CGCATGACATTGACCTCGGAGAATCTCGTGTGGTTATT 13
QQ	421	olysGlylleAlalleProHisAspIleAspLeuGlyGluSerArgValValll
Š	1321	AACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC 1.
qq	441	ofyraspasnglnHisGluGlnAspargProThrProSerProAlaProSerArg 46
ò	1381	GCTCTCTCTCACCGCTGCCGAGTAT 1.
qq	461	ropheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 48
ζŏ	1441	TATGTTTCTGACTCTGTGACCTTG
Dp	481	nSerThrTyrGlySerSerThrGlyProValTyrValSerAspSerValThrLeu 50
č	1501	GTTAATGTTGCGACGCGCGCGGCGCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACA 1560
qq	501	alAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr 52
ζ	1561	ف
qq	521	euAspGlyArgProLeuSerThrileGlnGlnTyrSerLysThrPhePheValLe
λõ	1621	CICCGCGGTAAGCICTCTTICTGGGAGCAGGCACACATAAAGCCGGGTACCTTATAAT 1680
qq	541	JArgGlyLysheuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTy
0y	1681	GACCAACTGCTTGTCGAGAATGCCG
qa	561	Argval
٥x	1741	ATTICACTIACACCATAGCCIGGGIGCIGGICCCGICICCAITICIGCGGITGCCGIT 1800
qq	581	leSerThrTyrThrThrSerLeuGlyAlaGlyProValSerIleSerAlaValAlaVa
λ	1801	CTGCGCTACCATTGCTTGAGGATACCTTGGACTACCCTGCCGCGCC 18
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OTHER INFORMATION: Synthetic construct
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Sequence 1. Application US/10257044

Publication No. US20030220475A1

GENERAL INFORMATION:

APPLICANT: The Government of the United States of America, as

APPLICANT: Human Services, Centers for Disease Control and Prevention

APPLICANT: HUMARD A. FIELDS

APPLICANT: HUMARD A. FIELDS

APPLICANT: VURL E. KHUDYAKOV

APPLICANT: VURL E. KHUDYAKOV

TITLE OF INVENTION NEUTRALIZING IMMUNOGENIC HEV POLYPEPTIDES (HEV)

TITLE OF INVENTION NUMBER: US/10/257,044

PRIOR PAPLICATION NUMBER: 60/195,380

PRIOR PAPLICATION NUMBER: 60/195,380

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FRASEEQ for Windows Vergion 4.0

SEQ ID NO 1

LENGTH: 660
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Best Local Similarity:
Query Match:
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US-10-257-044-1
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             MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                             3.81e-229
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TOPOLOGY: linear
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                                              LeuArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsn
                                                                                                                                                         TyrAsnThrThrAlaSerAspGlnLeuLeuValGluAsnAlaAlaGlyHisArgValAla
                                                                                                                                                                                                                                                      TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC
                                                                                                                                                                                                                                                                      ValAsnValAlaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpThrLysValThr
                                                                                                                                           TATAACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCGGGCACCGGGTCGCT
                                                                                                                                                                                                 ATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTCTCCATTTCTGCGGTTGCCGTT
                                                                                                                                                                                                                Yarbough, Patrice O.
Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 14:
    SEQUENCE CHARACTERISTICS:
    LENGTH: 660 amino acids
    TYPE: amino acid
    STRANDEDNESS: Hepatitis E Virus (Mexico Strain)
    ORF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (415) 324-0860
TELEFRAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/769,066
FILING DATE: 24-Jan-2001
CLASSIFICATION: CURROWD.>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/542,634
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McAtee, C. Patrick
Yarbough, Patrice O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09769066
Patent No. US20020107360A1
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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US-09-769-066-14
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Krawczynski, Krzysztof Z.
DF INVENTION: Hepatitis E Virus Vaccine and Method
OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
ENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,868
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
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NO: 20:
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Matches:
Conservative:
Mismatches:
Indels:
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STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,875
REGISTRATION NUMBER: 33,875
TELECOMMUNICATION INFORMATION:
TELEFPHONE: (415) 324-0860
TELEFRAX: (415) 324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
FILING DATE: 11-APRIL-1989
FILING DATE: 11-APRIL-1989
FILING DATE: 11-APRIL-1989
                                                                          5-10-105-00-2.0
Sequence 20, Application US/10165868
Publication No. US20030143241A1
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
Bradley, Daniel W.
                                                                                                                                                    Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: ORF
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 659 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20:
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3194.50
96.21%
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87.54%
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                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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STATE: CA
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Best Local Similarity:
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DB:
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                                                                   GACTITIGCCCTTGAGCTTGAGTTTCGCAACCTTACCCCCGGGTAACACCAATACGCGGGTC
                                                                                    CTCACCACCACGGCTGCTACCCGCTTTATGAAGGACCTCTATTTTACTAGTACTAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCAGCCCCATCGCGC
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 à a	1 MetArgProArgProLeuLeuLeuLeuLeuDheLeuDroBroketLeuDroAlaPro 20	Db 360 ValGlyGluValG	
 λ	CCGCCCGGTCAGCCGTCTGGCCGTCGTGGGCGCGCAGCGGCGGGGTTCCGGCGGTGGT	Oy 1141 GGGGCCTGCCGA 	GGCGGCCTGCCGACAGAATTGATTTCGTCGCCTGC 
 da ,	ProThrGlyGlnProSerGlyArgArgArgGlyArgArgSerGlyGlyThrGlyGlyGly	-	AATGGCGAGCCGACTGTTAAGTT
 à d	121 TTCTGGGGTTGGTTGTTCTCGGCCCTTCGCAATCCCCTATATTCATCCAAC 180 41 PhetrpGlyAspArgValAspSerGlnProPheAlaileFroTyrileHisProThrasn 60		
 Š	CCCTTCGCCCCGATGTCACCGCTGCGGCCCGGGCTGGACCTCGTGTTCGCCAACCCGCC	Qy 1261 CAGGATAAGGGTA            	CAGGATAAGGGTATTGCAATCCCGCATGACATTGA 
 QQ	61 ProbheAlabroAspValAlaAlaAlaSerGlySerGlyProArgLeuArgGlnProAla 80	1321	AACCAACATGAACAAGATCGGC
 රි සි	241 CGACCACTCGGCTTCGCTTGACCAGGCCCAGCGCCCGCCGTTGCCTCACGTCGT 300	440	
 2 2		Qy 1381 CCTTTCTCTGTCC	CCTTTCTCTGTCCTTCGAGCTAATGATGTGCTTTTC
 ga Qa		460	LeuArgAlaAsnAspValLeuTi
 ò	361 CCAGTGCCTGATGTCGACTCCGGGGGGCGCCATCTTGCGCCGGCAGTATAACCTATCAACA 420	Oy 1441 GACCAGTCCACTT 	GACCAGTCCACTTATGGCTCTTCGACTGGCCCAGT
 ą	121 ProvalProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140	1501	ACCRECECTAGE THE COLOR
 δλ	TCTCCCCTTACCTCTTCCGTGGCCACCGGCACTAACCTTCTTTTATGCCGCCCTCTT	•	500 ValAsnValAlaThrGlyAlaGlnAlaValAlaAr
 qq	41 SerProLeuThrSerSerValAlaSerGlyThrAsnLeuValLeuTyrAlaAlaProLeu	Qy 1561 CTTGACGGTCGCC	CCCCTCTCCACCATCCAGCAGT
 ඊ සී	481 AGTCGGCTTTAACCCTTCAGGACGGCACCAATACCCATATAATGGCCACGGAACGACGCATTT 540 :::	520	
λŏ	AATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCCGC	1621	CTCCGCGGTAAGCTCTTTTTGGGAGGCAGCAC
ДQ		540	LeuSerPheTrpGluAlaGlyTl
δ	601 GCTGTCGGCGGTTACGCCATCTCCATTCTGGCCACAGACCACCACCCCCGACG 660	09 1681 TATACACCACTG	
qa	201 AlaValGlyGlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThr 220	1741	ACCACTAGCCTGGGTGCTGGTCC
ò	661 TCCGTIGATATGAATTCAATAACCTCGACGGATGTTCGTATTTTAGTCCAGCCCGGCATA 720	580	
q	221 ServalaspMetAsnSerileThrSerThrAspValargileLeuValGinProGlyile 240	1801	rctgcgctagcattgcttgagg
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දු අධ	ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle	Db 620 HisThrPheAspA	AspPheCysProGluCysArgA.
ò		1921	CAGTCTACTGTCGCTGAGCTTCAGCGCCTTAAGAT
qa		Db 640 GlnSerThrValA	41aGluLeuGlnArgLeuLysVa
8 6	901 GACTTTGCCCTTGAGCTTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC 960 	KESULI 8 US-10-239-090A-57 ; Sequence 57, Application US/10239090A . Dublication No. HS20040101820A1	US/10239090A
3 8	からだされたからならればしてもられているかとなからいできます。 The Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholistic Substitution Cypholis	GENERAL INFORMATION:	TENT TO CHIES
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 ò	0-	; FILE REFERENCE: 02S0741P	secting hepatitis E vin
 •		COKKENI AFFLICATION NUMB	3EK: US/10/239,090A

primer derived from hepatitis E virus co luding the same, kit including the same, irus using the same CTGTTCAACCTTGCTGACACTCTGCTT 1140 GATACCTTGGACTACCCTGCCGCGCC 1860 GGTGGCCAGCTGTTCTACTCCCGTCCC 1200 STITATGITTCTGACTCTGTGACCTTG 1500 TACTCGAAGACCTTCTTTGTCCTGCCG 1620 cccercretriring contraction 1800 SACCTCGGAGAATCTCGTGTGGTTATT 1320 CCGACGCCTTCTCCAGCCCCATCGCGC 1380 IGGCTCTCTCTCACCGCTGCCGAGTAT 1440 ACAACTAAAGCCGGGTACCCTTATAAT 1680 SAGAATGCCGCCGGGCACCGGGTCGCT 1740 CCCCTTGGCCTTCAGGGCTGCGCTTTC 1920 ThrThrLysAlaGlyTyrProTyrAsn 559 GluAsnAlaAlaGlyHisArgValAla 579 AlaLeuGlyLeuGlnGlyCysAlaPhe 639 340 LeuThrThrAlaAlaThrArgPheMetLy8AspLeuHisPheThrGlyLeuAsnGly 359 g

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                                GACTITIGCCCTIGAGCTIGAGTTICGCAACCTTACCCCCGGTAACACACAATACGCGGGTC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT FILING DATE: 2003-07-24
PRIOR PAPLICATION NUMBER: JP2001-191837
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 57
LENGTH: 674
TYPE: PRI
                                                                                  4.84e-226
3179.00
95.90%
92.11%
87.12%
                                                   GRGANISM: Hepatitis
US-10-239-090A-57
                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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HisThrPheAspAspPheCysProGluCysArgThrLeuGlyLeuGlnGlyCysAlaPhe
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TITLE OF INVENTION: Polynuclectide probe and primer derived from 1
TITLE OF INVENTION: from Japanese, chip including the same, kit:
TITLE OF INVENTION: detecting hepatitis E virus using the same
FILE REFERENCE: 0280741P
CURRENT APPLICATION NUMBER: US/10/239,090A
CURRENT FILING DATE: 2003-07-24
PRIOR PILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 519
                                                                                                                                                                                                                                                                                                                                                  (1-1983) x US-10-239-090A-51 (1-660)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                        RESULT 9
US-10-239-090A-51
Sequence 51, Application US/10239090A
Publication No. US20040101820A1
GENERAL INFORMATION:
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3176.00
96.05%
92.11%
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                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Hepatitis
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                                                                                                                                                                                                                                                                                                  Percent Similarity:
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Pred. No.:
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EARLIER APPLICATION NUMBER: US 09/173,141
EARLIER FILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: US 60/061,199
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 258
SOPTWARE: FASTSEQ for Windows Version 3.0
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95.75%
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                                                                                       ValValSerAlaAsnGlyGluProThrValLysLeuTyrThrSerValGluAsnAlaGln
                                                                                                                                                                                                                                                                                                               GITGICTCAGCCAATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAG
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Fublication No. US20030049601A1
GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION: HEPATITIS E VIRUS
TITLE OF INVENTION WUMBER: US/09/468,147A
CURRENT APPLICATION WUMBER: US/09/468,147A
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Qy 1801 TTAGCCCCCCACTCTGCCCTAGCATTGCTTGACATACCTTGGCCCCGCCC 1860  bb 601 LethlaProHisSerAlaLeuAlaValhaValhapThrValAspTyreDAlaArgAla 620  Cy 1861 CAACTTTTGATGATTTCTGCCCCCCCTGCCCCCTTGGCCTTC 1920  Cy 1921 HisThrPheAspaspPhcYsProdlucysAgThrLeuGlyLeuGlnGlyCySalaPhe 640  Cy 1921 CAGTCTACTGTCGCTGACCTTCAGGCCTCCCCTTGAGGCTTCCGGGTTC 1920  Cy 1921 CAGTCTACTGTCGCTGACCTTCAGGCTTAGATGAAGGTGGGTTAAAACTCGGGAG 1977  Db 641 GINSerThrIleAlaGluLeuGlnArgLeuLySMetLySValGlyLySThrArgGlu 659  RESULT 13  US-10-119-745-92  Sequence 92, Application US/10319745  Sequence 92, Application US/10319745  Sequence 92, Application US/10319745  APPLICANT: Schlauder, George G.  APPLICANT: Schlauder, George G.  APPLICANT: Besai, Suresh M.  APPLICANT: Dawson, George G.  APPLICANT: Dawson, George G.  APPLICANT: Dawson, George G.  APPLICANT: Dawson, George G.  APPLICANT: MEMBATWAR: I. K.  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  TITLE OF INVENTION: METHODS AND COMPOSITION NUMBER: US 09/173,141  PRIOR PILING DATE: 2002-12-21  PRIOR PILICATION NUMBER: BALLIER APPLICATION NUMBER: US 60/061,199  PRIOR PILING DATE: EARLIER FILING DATE: 1999-10-15  PRIOR PILING DATE: EARLIER FILING DATE: 1997-10-15	SOFTWARE   Part RECORD   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION
GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACATTGTAACCAAGGCTGGGGCTCC 78 AlaSerGluLeuValileProSerGluArgleuHisTyrArgAsnGlnGlyTrpArgSer 26 GTCGAGACCTCTGGGTGGCTGAGGGGGGGTGCTTTGTTATGCTTTGCATA 84 ValGluThrThrGlyVallalaGluGluAlaThrSerGlyLeuValMetLeuCysile 28 CATGGCTCACTCGTAAATTCCTAAACTACACCTATACCGTGGGGTGTTG 90 HisGlySerProValAsnSerTyrThrAsnThrProGlyAsnThrAsnThrAsylleuUeu 30 GACTTGCCTTGAGCTTGGGAACCTTACCCGGTGACCCAATACGGGGGTGTTG 90 HisGlySerProValAsnSerTyrThrAsnThrProGlyAsnThrAsnThrAsyll 32 TCCCGTTAATTCCAGCACGCTGCCCCGGTAACCCCAATACGCGGGTGTG 96 ASPPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrAsyll 33 TCCCGTTAATTCCAGCACCTGCCCCGCTTACCCCGGTGACCCAATACGCGGGTG 96 ASPPheAlaLeuGluLeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrAslaGlu 34 CTCACCACCACCACGGCTGCCCCCCCTTAATTTACTAGTACTAATGGT 10 LeuThrThrThrAlaAsTATAAGAAGGACCTTAATTTACTAGTACTAATGGT 36 LeuThrThrThrAlaAlaArgHisArgAstGaCCTCTAATTTACTAGTACTAATGGT 36 LeuThrThrThrAlaAlaArgHisArgAstGaCCTCACTCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACCTGTGACTGTGACTGTGACTGTGACTGTGACTGTGACTGTGACTGTGTGTG	401 Valvalseralashidilililililililililililililililililili

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ignment Scores: 5.63e-224 Length: 660 ore: 3151.00 Matches: 603 ore: 3151.00 Matches: 26 conservative: 26 st Local Similarity: 91.50% Mismatches: 30 ery Match: 10 Gaps: 0 10 Gaps: 0 -09-851-410A-6_COPY_5147_7129 (1-1983) x US-09-468-147-167 (1-660)	Qy         1 ATGCGCCGTCGGCCGATTTTGTTGCTGCTCTAATTTTTGCTGCCGGGCA 60	QY         121 TTCTGGGGTGACCGGGTTGATTCTCAGCCCTTCGCAATCCCCTATATTCATCCAACCAA	241 CGACCACTCGGCTCGCGTTGGCGGGCCCAGCGCCCCGCCGTTGCCTCACGTCGT [	Qy         301 AGACCTACCAGCTGGGGCCGCTGCTAACCGGGCTCGCCCATGACACCCCG         360           Db         101 ArgSerAlaProAlaGlyAlaAlaProLeuThrAlaValSerProAlaProAspThrAla         120           Qy         361 CCAGTGCCTGATGTCGACTCCGGGGGCCATCTTGGGCGGGGTATAACCTATCAACA         420	Db 121 ProValProAspValAspSerArgGlyAlaIleLeuArgArgGlnTyrAsnLeuSerThr 140  Qy 421 TCTCCCCTTACCTCTTCCGTGGCCACCGGCACTAACCTGGTTCTTTATGCCGCCCTCTT 480	Qy 481 AGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCCACGGAAGCTTCT 540 :::	Qy         541 AATTATGCCCAGTACCGGTGCCACAATCGGTTACCGCCGGTGGTCCCCAAT         600           Db         181 AsnTyrAlaGlnTyrArgValValArgAlaThrIleArgTyrArgProteuValProAsn         200           Qy         601 GCTGTCGGCGGTTACGCCATCTCATTCTGGCCACAGACCACCCCGACG         660           C         61 GCTGTCGGCGGTTACGCCATCTCATTCTGGCCACAGACCACCCCCGACG         660	661 TCCGTTGATATCAATAACCTCGACGGATGTTCGATTTTAGTCCAGCCCGCGTA	Oy 721 GCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCGTAACCAAGGCTGGCGCTCC 780	Qy         781 GTCGAGACCTCTGGGGTGGCTGAGGAGGAGGTACCTCTGGTCTTGTATGCTTTGCATA 840           Db         261 ValGluThrThrGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 280	OY 841 CATGGCTCACTCGTAAATTCCTATACACCCTATACGGGGGCCCTCGGGCTGTTG 900	Qy 901 GACTITGCCCTTGAGCTTCGCAACCTTACCCCCGGTAACACCAATACGCGGGTC 960

Db	301	AspPheAlaLeuGlubeuGluPheArgAsnLeuThrProGlyAsnThrAsnThrArgVal 320
ò	961	TCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACGGGACTGCC
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λŏ	1381	CTCACCGCTGCCGAGTAT 14
Dβ	461	roPheSerValLeuArgAlaAsnAspValLeuTrpLeuSerLeuThrAlaAlaGluTyr 4
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qq	481	SerSerThrAsnProMetTyrValSerAspThrValThrLeu 5
ò	1501	GTTAATGTTGCGACCGGGCGCGGGCGTTGCCCGGTCGCTCGATTGGACCAAGGTCACA 1560
QQ	501	S
δ	1561	CTTGACGGTCGCCCCTCTCCACCATCCAGCAGTACTCGAAGACCTTCTTTGTCCTGCCG 1620
qq	521	LeuAspGlyArgProLeuThrThrIleGlnGlnTyrSerLysThrPheTyrValLeuPro 540
ò	1621	CTCCGCGGTAAGCTCTCTTTCTGGGAGGCAGGCACAAAAGCCGGGTACCCTTATAAT 1680
οp	541	-ניז
λΌ	89	17
DÞ	نو:	IleGluAsnAlaAlaGlyHisArgValAla 58
δλ	1741	SGICCCGICICCATITICIGCGGIIGCCGII 18
ΩÞ	581	lleSerThrTyrThrThrSerLeuGlyAlaGlyProThrSerIleSerAlaValGlyVal 600
٥٨	1801	TTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACCTTGGACTACCCTGCCCGCGCC 1860
οgα	601	
δ	1861	CATACTTTTGATGATTTCTGCCCAGAGTGCCGCCCCTTGGCCTTCAGGGCTGCGCTTTC 1920
qq	621	AlaPhe 64
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schlauder, George G.
APPLICANT: Schlauder, George G.
APPLICANT: Erker, James C.
APPLICANT: Besal, Suresh M.
APPLICANT: Desal, Suresh M.
APPLICANT: Desal, Suresh M.
APPLICANT: Dawson, George J.
APPLICANT: Dawson, George J.
APPLICANT: Mushahwar, I. K.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING TITLE OF INVENTION: HEPATITIS E VIRUS
FILE REFERENCE: 632-US-P1
CURRENT APPLICATION NUMBER: US/10/319,745
CURRENT APPLICATION NUMBER: US/09/468,147A
PRIOR APPLICATION NUMBER: BALLIER APPLICATION NUMBER: US/PRIOR PELING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: ERALIER APPLICATION NUMBER: US/PRIOR PELING DATE: EARLIER FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 167
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Search completed: August 16, 2004, 13:33:17 Job time: 137.324 secs

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APPLICANT: ADAMS, Mark
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: OFFURE AGENTS, AND USES THEREOF
FILE REFERENCE: CLOO1381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
SEQ ID NO 55792
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Best Local Similarity:
  RESULT 1
US-10-170-205E-35792
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-Q=/Cgn2 1/USPTO spool p/US09551410/runat 16082004 125455 8586/app_query.fasta_1.4238
-Q=/Cgn2 1/USPTO spool p/US09551410/runat 16082004 125455 8586/app_query.fasta_1.4238
-Q=/Cgn2 1/USPTO spool p/US09551410/runat SURTEX=n2p.rapn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRART=1 -END=-1 -MATRIX=blosum62
-TRANS=bluman40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINIEN=0
-MAXIEN=200000000 -USER=US09851410 @CGN 1 1 395 @runat 16082004 125455 8586
-NCPUE 6 -ICPU-3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT - DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 7551, Ap
Sequence 7551, Ap
Sequence 19858, A
Sequence 1197, Ap
Sequence 185, App
Sequence 280165,
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1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US07_NEW COMB.pep:*

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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-170-205E-19858
US-60-581-351-7586
US-60-581-351-7586
US-60-591-969-185
US-10-425-115-280165
PCT-USO2-205E-18975
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	CAGCCCTTCGCAATCCCCTATATTCATCCAACCAACCCCTTC   ::	GCCCCCGGATGTCACCGCTGCGGCGCTGGACCTCGTGTTCGCCAACCGGCCGACCA	CTCGGCTCCGCTTGGCGTGACCAGCCCCGCCGCTTGCCTCTCGCTGTTGCCTCTTGCCTTTGCCTTTGCTCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTTGCTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTGCTTTTTGCTTT	ACCACAGCTGGGGCGGCGGCTAACGGGGGGTGG	CATGACACCCGGCCAGTGCCTGATGTCGACTCCCGCGGCGCCATCTTGGGCCGGCAGTAT 4	AACCTATCAACATCTCCCCTTACCTCGTGGCCACCGGCACTAACCTGGTTCTTTAT 4	GCGGCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGCACCAATACCCATATAATGGCC	ACGGAAGCTTCTAATTATGCCCAGTACCGGGTTGCCCGTGCCACAATCCGTTACCGCCG ::::::::::::::::::::::::::::::::	CIGGTCCCCAATGCTGGGGGGTTACGCCATCTCCATCTCATTCTGG 6	CCACAGACCACCACCACCACCCCGACGTCCGTTGATATGAATTCAAT 6 :: : :: :: :: :: :: :: rSerGlnThrProGlyHisProLeuLeuAlaProThrSerSerHisValProGlyLe 1	AACCTCGACGGATGTTCGTATTTTAGTCCAGCCGGCATAGCCTCTGAGCTTGTGATCCC 7	AAGTGAGCGCCTACA 7	CTATCGTAACCAAGGCTGGCGTCCGTCGAGGCTCGGGGTGGCTGAGGAGGAGGCTAC :::::::       ::	CTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCTATACTAATACACC 8	CTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGCAACCTTAC 9	CCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCTCGCCACCGCCTTCG 9	TCGCGGTGCGGACGGGACTCCCGAGCTCACCACCACCGCTG	

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41	qq	694 lThrSerAlaAspGlyProValP
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2 4	qq	714 lThrSerAlaAspSerServalPh
1 2	ζŏ	1684 AACACCACT
	qq	734 IThrProAlaAsnAspProValVa
	δλ	1727GGCACCGGGTCGCTAIT
8 4	qq	   754   SerSerAlaAspG yProlleVa
	δλ	1780 TCCATTTCTGCGGTTGCCGTTTTA
	QQ	   774  ThrThrAlaAspAspProIle
PVallage Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular Asp Particular A		343 453 359 379 573 399 633 418 693 450 810

qu	465	3 46
δλ	871	RACCGGIGCCTCGGGCTGTTGGACTTTGCCCTTGAGCTTGAGTTTCGC 92
qq	469	alprovalThrProThrAspPheProValValAlaValThrProAlaAs
٥x	928	C 98
qq	489	rThrvalAspProvalThrProAlaAspGlyProvalvalProval 504
٥٨	988	CACCACCACGGCTGCTACCCGCTTT 10
qq	505	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ζö	1048	AIGAAGGACCTCTATTTACTAGTACTAATGGTCGGTGAGATCGGCCGCGGGATAGCC 1107
qq	511	-AspAsp
ò	1108	TCACCCTGTTCAACCTTGCTGACACTCTGCTGGCGGCCTGCCG 11
qq	521	ProvalThrPro-AlaAspSerLeuIleValSerValThrProAlaAspS
δλ	1153	ACAGAATTGGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCC 1212
qq	541	alThrProAlaAspGlyArgValIleProValAlaSerAl
δλ	13	AATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGGAT 1266
qq	558	 AspSerProIleValProValThrProAlaAspThrValValValProValThrProAla 577
λo.	_	CAATCCCGCATGACATTGACCTCGGGGAATCTCGTGTGGTTATTCAG 1:
<b>q</b>	578	eProValThr 59
δ	1324	GATTATGATAACCAACATGAACAAGATCGGCCGACGCCTTCTCCA 1368
Dp	596	ProValAspSerProValValProValThrSerAlaAspSerProLeuIleProValThr 615
λ̈́O	1369	GCCCATCGCGCCTTTCTCTTCTGGGCTAATGATGTGCTCTTGGCTCTCTCT
Db	919	ValPro
٥'n	1426	ACCGCTGCCGAGTATGACCAGTCCACTTATGGCTCTTCGACTGGCCCAGTTAT 1479
qq	635	
ò	1480	GTTTCTGACTCTGTGACCTTGGTTAATGTTGCGACCGGCGCGCGC
qq	655	Pro
λ	1534	CGGTCGCTCGATTGGACCAAGGTCACATGACGGTCGCCCCTCTCCACCATC 1587
QQ	675	ThrserAlaAsp-GlyProValValSerIleThrProAlaAspSerProValPheProVa 694
λ̈	1588	CAGCAGTACTCGAAGACCTTCTTTGTCCTGCCGCTCCGCGGTAAGCTCTCT 1638
DP	694	alPr
ò	1639	TICTGGGAGGCAGGCACAACTAAAGCCGGGTACCCTTATAATTAT 1683
Dp	714	lthrSerAlaAspSerSerValPheProValThrThrAlaAspGlyProValValProVa 734
ò	1684	AACACCACTGCTAGCGACCAACTGCTTGTCGAGAATGCCGCCG 1726
ηρ	734	AsnAspPr
δλ	1727	GGCACCGGGTCGCTATTTCCACTTACACCACTAGCCTGGGTGCTGGTCCCGTC 1779
අු	754	erSerAlaAspGlyProlleValProValThrProAlaAspS
δλ	1780	1CCATITCTGCGGTTGCCGTTTTAGCCCCCCACTCTGCGCTAGCATTGCTTGAGGATACC 1839
q _Q	774	lThrThrAlaAspAspProlleValPr 783

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1149 GCCGACAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCG------TCCCGT 1202
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                      318 SerAlaProValProGlyVal------ProLeuAlaProLeuProIleSerGlyArg 334
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                                                                                                                              702 ITTAGTCCAGCCCGGCATAGCCTCTGAGCTTGTGATCCCAAGTGAGCGCCTACACTATCG 761
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 CCGCCCGCTGGTCCCCCAATGCTGTCGGCGGTTACGCCATCTCCATCTCATTCTGGCCACA
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-----LysGluThrProProAlaProProAlaPro-----
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
LENGTH: 763
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-----ProPheProProValProProAlaProProAlaArgGlu 75
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LeuAlaProProLeuProProAlaProProGluAlaProArgGluSerArgProAlaLeu 95
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                  ------PheProProAlaAlaLeuAsnProProAlaProProAla--
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TIGGACTACCCTGCCCGCCCCATACTTTTGATGATTTCTGCCCAGAGT
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Matches:
Conservative:
Mismatches:
Indels:
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; Sequence 7551, Application US/60581351
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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US-60-581-351-7551
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Pred. No.:
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Plants

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466 TATGCCGCCCCTCTTAGTCCGCTTTTACCCCTTCAGGACGGCACCAATACCCCATATAATG 525
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In J
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In J
FILE REFERENCE: 38-21 (53372 B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR FILING DATE: 2003-66-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SEQ ID NO 7586
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                   1882 CCAGAGTGCC---GCCCCCTTGGCCTTCAGGGCTGCGCTTTCCAGTCTA 1927
                                     ---- ProAspArgIleProProAlaPro-
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                                                                                      -----ATGTCACCGCTGCGGCCGGGGCTGGACCTCGTG
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                                                                                                                                      TTCGCCAACCCGCCCGACCACTCGGCTCCGCTT----GGCGTGACCAGGCCCAGCGCCCCG
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             US-09-851-410A-6_COPY_5147_7129 (1-1983) x US-60-591-969-185 (1-5179)
                                    CTCAGCCCTTCGCAATCCCCTATATTCATCCAACCA-
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Sequence 280165, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)B
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1860 alileProMetAlaPheCysLeuAsnTyrGluIleAsnValGlnCysCysGluCysValT 1880
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                                                          1154 CAGAATTGATTTCGTCGGCTGGTGGCCAGCTGTTCTACTCCCGTCCCGTTGTCTCAGCCA 1213
                                                                                                                 --ProGlyTrpAlaAlaA 1820
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2014 ThrProlleThrThrThrThrValThrProThrPro-
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974 GCACTGCTCGCCACCGCCTTCGTCGCGGTGCGGACTGCCGAGCTCACCACCACCACGG 1033
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232 LeubroSerProProValGlnGlnProProArgThrProlleLeuProProSerArgLys 251
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                                                                                 863 ATACTAATACACCCTATACCGGTGCCCTCGGGCTGTTGGACTTTGCCCCTTGAGCTTGAGT
      803 AGGAGGAGGCTACCTCTGGTCTTGTTATGCTTTGCATACATGGCTCACTCGTAAATTCCT
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Matches:
Conservative:
Mismatches:
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Gaps:
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CURRENT PEDLICATION NUMBER: PCT/US02/22858A CURRENT FILING DATE: 2002-07-19
PRIOR PEDLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-02-03
PRIOR PILING DATE: 2000-03-07
PRIOR PAPLICATION NUMBER: US 09/515,126
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
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PRIOR FILING DATE: 2000-03-07
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PRIOR FILING DATE: 2000-05-18
PRIOR PELING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
                              223 -----IleProAlaProArgLeuGly--
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Yang, Yonghong
Weng, Gezhi
Zhang, Jie
Ren, Felyan
Xue, Aidong J.
Wang, Jian-Rui
Wehrman, Tom
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Zhao, Qing A.
Wang, Zhiwei
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Best Local Similarity:
Query Match:
DB:
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PCT-US02-22858A-249
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| ArgProProGlnLeuGlyAlaProLeuProThrProValAlaProThrProGlnLeuGlu 149
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52 ThrProArgProProGlyLeuGlyAlaProThrArgThrProPro------LeuPro
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117 ------ProArgValGlyAlaProSerProAlaProProProVal-------
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-----ArgSerProVallleProPro-----
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/10/425,115 CIRRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 280165 LENGTH: 321
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187.50
37.32%
28.28%
5.14%
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Best Local Similarity:
                                                                                                    TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                          FEATURE:
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Sequence 18875, Application US/10170205E

Sequence 18875, Application US/10170205E

Sequence 18875, Application US/10170205E

GENERAL INFORMATION:

APPLICANT: ADAMS, Mark

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF

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CURRENT APPLICATION NUMBER: US/10/170,205E

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CURRENT FILING DATE: 2002-06-13

NUMBER OF SEQ ID NOS: 40312

SOFTWARE: PATENTIN VEXSION 3.2

SEQ ID NO 18875

LENGTH: 5262
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	CTGCTACCGGTTTATGAAGGACCTCTATTATACTAGTACTAATGGTGTGGGGGATGTGGTGTGGTGTGGTGGTGGTGGT	1214 ATGGCGAGCCGACTGTTAAGTTGTATACATCTGTAGAGAATGCTCAGCAGATAAGGGTA 1273	
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Db 902 GlyGlnGlySerProCysGluGluGluBroArgAlaProValAla 918  Qy 1772 GTCCGTCTCCATTTTGCGGTTGCGGTTTTAGCCCCCACTTG 1816	ignment Scores:  o.000527 Length: 5262  da. No.:  182.00 Matches: 138  reent Similarity: 22.37% Mismatches: 176  st Local Similarity: 22.37% Mismatches: 176  ery Match: 6  o.9-851-410A-6_COPY_5147_7129 (1-1983) x US-10-896-891-303 (1-5262)  149 CCTTCGCAATCCCTATATTCATCCAACCAACCCCTGCGCGATGTCGGGG	TTCGCCAA :: ProleuSe CCGTTGC     Pro CGGCCCAT	

308 CCACAGCTGGGGCCGCCTAACCGCGGTCGGCCCATGACACCCCGCCCAGTGC	#82 GICCGUITIACCCUTTCAGAGAGACGATTCATAGAGAGAGAGAGAGAGAGAGAG	617 594 662 614 707	b 630 SerSerProValAlaSerAlaMetHisAlaLysValThrProArgProLeuProAlaSer 649  716	821 GTCTTGTTATGCTTTGCATGCCTCACTCGTAAATTCCTATACTA 821 GTCTTGTTATGCTTTGCATACATGCCTCACTCGTA	y 929 ACCTTACCCCGGTAACACCAATACGCGGGTCTCCCGTTATTCCAGCACTGCCCCCC 988	1049 TGAAGGACCTCTATTTACTAGTACTAATGGTGTGAGATCGCCGGGGATAGCCC 1108
6 6 6 6 6	86868	8 8 8 8	4 6 6 6	8 6 8 6	8 6 8 6	8 6 8 6 8
B68SerLeuAlaSerGluLeuLysGlySerProValLeuLeuAspProGlu 883	RESULT 12 US-10-851-438-79 Sequence 79, Application US/10851438 GENERAL INFORMATION APPLICANT: Curaden Corporation APPLICANT: Vernet, Corine A.M. APPLICANT: Fernandes, Elma R APPLICANT: Taupier, Raymond J APPLICANT: Quinn, Kerry E APPLICANT: Spytek, Kimberly A	APPLICANT: Herrman, John L APPLICANT: Herrman, John L ATTLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same FILE REPRENCE: 15966-750 CURRENT APPLICATION NUMBER: US/10/851,438 CURRENT FILING DATE: 2004-05-21 PRIOR APPLICATION NUMBER: 60/194,314 PRIOR APPLICATION NUMBER: 60/194,314 PRIOR APPLICATION NUMBER: 60/194,314	FRIOR FILING DATE: 2000-08-16  NUMBER OF SEQ ID NOS: 85  SOFTWARE: Patentin Ver. 2.1  SEQ ID NO 79  LENGTH: 1151  TYPE: PRT  ORGANISM: Gallus gallus  US-10-851-438-79	ty: arity	19-851-410A-6_COFT_5147_729 (1-1983) X US-10-851-438-79 (1-1151)	Db 410ProAlaAlaAlaAlaProGlnGlnProValProLysAlaAlaProVal 424  182CCTTCGCCC

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0.000402
180.00
32.72%
23.70%
4.93%
         FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(708)
OTHER INFORMATION: un
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Best Local Similarity:
Query Match:
DB:
Zea mays
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Pred. No.:
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: A Royal M.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 313976
LENGTH: 708
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                     laThrGlnValThrAla-----ThrSerAlaGlyAsnThrMetGlnValSerProM 808
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826 lnProSer-ProMetGlyAlaAlaThrThrLeuMetSerProMetGlyAlaAlaThrThr 845
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31 Proval------GlySerProProProProValLysThrThrSerProProAlaPro 47
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Matches:
Conservative:
Mismatches:
Indels:
                                        ; OTHER INFORMATION: Clone ID: MRT4577_49406C.1.pep
US-10-425-115-313976
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unsure at all Xaa locations
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Sequence 260103, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cavalic, David K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-2.1(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/260103
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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Mismatches:
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OTHER INFORMATION: unsure at all Xaa locations
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Matches:
              1870 GATGATTTCTGCCCAGAGTGCCGCCCC 1897
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Query Match:
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ORGANISM: Zea mays
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99 CTTTTACCCCTTCAGGACGCACCAATACCCATATATGGCCACGGAAGCTTCTAATTAT 546  133	Sequence   1484, Application   US/10170205E   Sequence   1484, Application   US/10170205E   Sequence   1484, Application   US/10170205E   Sequence   1484, Application   US/10170205E   Septicant's Abars, mark

2 CTGAGGAGGAGGCTACCTCTGGTTTTTATATATATATATA	772	1Pro 786	858	962		AACCTTACCCCC 939                 Db aThrLeuPro 832	696		3GGACTGCCGAG 1020	SerGlnAlaGly 872	AGTACTAATGGT 1080	Ser 889	1122	3lnAlaProLeu 909			ACATCTGTAGAG 1251	SGAGAATCTCGT 1311	086	JCT 1362	 	CTTTGGCTCTCT 1422	rhrTyrSer 1008	CAGTTTATGTT 1482	:::        3er-GlyArgPr 1045	CAGTACTCGAAG 1602	ValArgGl 1060	GCACAACTAAA 1662	oThrProProAl 1076	ספאו ההמהמתבת מתרמת המהת
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 Command line parameters:
-MODEL=frame+ n.p.model -DEV=xlp
-MODEL=frame+ n.p.model -DEV=xlp
-Gen2_1/USFTO_spool_p/US09851410/runat_16082004_125716_9617/app_query.fasta_1.4238
-D=A_Gen2_2_1/USFTO_spool_p/US09851410/runat_16082004_125716_9617/app_query.fasta_1.4238
-D=A_Geneseq_29Gan04 -OFMN=fastan -SUFFIX=oli.rag -MINMATCH=0.1 -LOOPCL=0
-LIST=45 -DOCALIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USFR=45 -DOCALIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USFR=45 -DOCALIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USFR=US09851410_@CGN 1 1.141_@runat_16082004_125716_9617 -NCPU=6 -ICPU=3
-NO MARP -LARGEQUERY -NEG SCORES=0 -MALT -DSPBBLOCK=100 -LONGLOG
-DSP TIMEOUT=120 -WARN TIMEOUT=30 -THREADS-1 -XGAPOP=66 -YGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDP=6 -DELEXT=7
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Aaw93387 H
Aar96090 H
Aar96092 H
Aar96102 H
Aar96104 H
Aaw35821 H
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                    using frame_plus_n2p model
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                                   TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA
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                                                                       AlaProArgSerAlaLeuAlaLeuLeuGluAspThrPheAspTyrProGlyArgAlaHis 620
                                                                                                              virus; Burma; Mexico; immunoassay; peptide antigen; antibody;
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                                                                                                                                                                                                                                                                                       Hepatitis E virus Mexico strain protein from ORF2
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89US-00336672.
89US-00367486.
89US-00450921.
90US-00681078.
92US-00821378.
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diagnosis; HEV
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Mismatches:
Indels:
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Pred. No.:
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14-FEB-1994
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The sequence is that of the putative virus capsid protein encoded by Mexico strain hepatitis E virus (HEV) open reading frame ORF2. This protein or peptide fragments of it may be used in a vaccine composition for immunising an individual against HEV. Antibodies raised against these peptides can also be used in such vaccines. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                           Hepatitis E virus; vaccine; neutralising antibodies; infection; block; open reading frame; antibodies.
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Query Match:
DB:
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241 CGGCCACTTGGCTACGACTAGGCCCAGCCCCTCCGCTGCCTCCCGTCGC 300	ArgProAlaThrAlaG1yAlaAlaAlaLeuThrAlaValAlaProAlaHisAspThrSer CCCGTCCCGGACGTTGATTCTCGCGGGCGACGTTGATTTGTCTACT	121 ProvalProAspValAspSerArgGlyAlalleLeuArgArgGInIyrAsnLeuSerint 140 421 TCACCCCTGACATCCTCTGTGGCCTCTGGCATATTTAGTCCTGTATGCAGCCCCCTT 480	481 AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	541 AATTATGCACAGTACCCGCTTGCCCGCTACTATCCGTTACCGCCCCTAGTGCCTAAT 600 181 AShTyrAlaGlnTyrArgValAlaArgAlaThr11eArgTyrArgProLeuValProAsn 200	01	61 TCTGTTGACATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATA	21 GCATCTGAATTGGTCATCCCAAGCGGCCTTCACTACCGCAATCAAGGTTGGCGTCG	41 Alasetolubeuvalliefloseiglumigbeurisiyrrigasholmiryilpalgose 81 GTTGAGACATCTGGTGGTGGGGGAAGCCACCTCCGGTCTTGTCATGTTATGCATA 	TACTG	01 GACTITOCCTEAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACGCTGTGTG	961 TCCCGTTACTCCAGCACTGCTCGTCACCCCGAGGGGCCCGACGGGACTGCGGAGCTG 1020	1021 ACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTACCGGCCTTAATGGGGTA 1080 	1081 GGTGAAGTCGGCCGCGGGATAGCTCTAACGTTAACCTTGCTGACACGCTCCTCGGC 1140 	1141 GGGCTCCCGACAGAATTAATTTCGTCGGCTGGCGGCAACTGTTTTATTCCCGCCCG	1201 GTCTCAGCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGCTCAGCAG 1260	1261 GATAAGGGTGTTGCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAG 1320

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diagnosis, prevention and treatment of hepatitis B virus infection mammals, particularly humans. 

Example 1; Fig 3A; 70pp; English

This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine Strains of HEV. The swine HEV can also be used as a therapeutic treatment for infection by other attrains of HEV. The swine HEV can also be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or

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1621 CGTGGCAAGCTCCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT 541 ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyr

1561 GACGGGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCTT

560

1681 AATACTACTGCTAGTGACCAGATTCTGATTGAAAATGCTGCCGGCCATCGGGTCGCCATT 1740

388	products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection	음 &
ខ្លួ	a human virus and thus can be har	73
38	experimentally and clinically Without lear of severe infection and/or contamination	අ <u>ධ</u>
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HEV; enterically-transmitted non-A/non-B hepatitis virus; vaccine; diagnosis; antigen; Spodoptera frugiperda; Sf9; insect; baculovirus; capsid.
                                Hepatitis E virus (Mexico strain)
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62K antigen (AAR96092) comprises the C-terminal 549 amino acids of hepatitis B vinus (HEV) Mexico strain capsid protein (see also AAR96090). It is obtd. by PCR amplification of HEV Mexico ORF-2 (AAT27108), insertion of amplified DNA (AAT27110) into vector pGBX and expression in E. coli cealls. Expression of full-length ORF-2 in Sf9 insect cells using a haculovirus system also results in prodn. of 62K antigen (see also AAR96102 and AAR96104). 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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in vaccines
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                                                                                                             Yarbough PO,
                                                                                                                                                                                                                                                                                             Claim 4; Page 84-86; 125pp; English
                                                                  (GENE-) GENELABS TECHNOLOGIES INC
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95US-00542634.
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AAR96092

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DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus (HEV) Mexico strain capsid protein was cloned into baculovirus expression vector pBluBacIII and recombinant 62K was expressed in Sf9 insect cells. High levels of expression were obtd. and the recombinant 62K was obtd. in over 95% purity. However, C-terminal processing resulted in the deletion of 9 or 23 amino acids from 62K, giving 2 related polypeptide species (AAR96102 and AAR96101 and AAR96103). Recombinant 62K amitigen (see also AAR96101 and AAR96103). Recombinant 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                    TGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGG
                                     eGluksnAlaAlaGlyHisAxgValAlaIleSerThrTyrThrThrArgLeuGlyAlaGl
                                                                          TCCGGTCGCCATTTCTGCGGCGCGCGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGA
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and in vaccines
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Qy         1290 CGATCTTGGTGATTTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGGATCG 1349           Db         320 eAspLeuGlyAspSerArgValValIleGlnAspTyrAspAsnGlnHisGluGlnAspAr 340           Qy         1350 GCCCACCCCGTCGCGCCATCTCGGCCTTTTTCTGTTCTCCGAGCAAATGATGATCT 1409           Db         340 gProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLe 360           Qy         1410 TTGCTCTCTCTCTCTCTCTCTCTACTCACTCACTCACTCA	1470   11   1   1   1   1   1   1   1   1	Qy 1530 CCGATCGCTTGACTGGTCCAAAGTCACCTCGACGGGGGGGCCCCTCCCGACTGTTGAGCA 1589		1710	1770	1830	1890 CG 	Cy 1950 A 1950 Db 540 B 540	RESULT 8 AAR96104 ID AAR96104 standard; protein; 525 AA. XX	AC AAR96104; XX XD DT 16-OCT-2003 (revised) DT 06-AUG-1996 (first entry)	<pre>spatitis E virus (Mexico strain) recombinant 62</pre>	XX Mepatitis E virus; Mexico strain.	XX WO9612807-A2. XX YD 02-MAY-1996.	XX PF 23-OCT-1995, 95WO-US013703. XX PR 24-OCT-1994, 94US-00327952.
Alignment Scores:  Pred. No.:  Score:  Score:  Score:  Stock  Score:  392.00 Matches:  Score:  99.45\$ Conservative: 0  Best Local Similarity: 99.45\$ Mismatches: 1  Query Match:  29.48\$ Indels: 3  DB:  US-09-851-410A-10_COPY_5117_7096 (1-1980) x AAR96102 (1-540)	1 AlaValAlaProAlaHisAspThrSerProValProAspValAspSerArgGlyAlaile 94 CTACGCCGCAGTATAATTGTCTACTTCACCCCTGACATCCTCTGTGGCCTCTGGCACT	Decarger grant of the state of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of	514 ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCTACT 573	TGGCCTCAAACAACCACAACCCCTACATCTGTGACATGCATTACTTCCATTACTTCCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTGATTCACTACTACTACTACTACTACTACTACTACTACTACT	694 GTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCG	754 CACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCTGGTGTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	814 ACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCAGTTAACTCCTATACCAATACC 873 	874 CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTTCGCAATCTC 933 	934 ACCACTGTAACACCAATACACGTGTGTCCCGTTACTCCAGCACTGCTCGTCACTC 989	990 CGCCCGAGGGCCCGACGGGGAGCTGACACACACAGCCACCAGGTTCATGAA 1049 	1050 AGATCTCCACTTTACCGGCCTTAATGGGGTAGGTGAAGTCGGCCGCGGGATAGCTCTAAC 1109	ATTACTTAACCTTGCTGACACGCTCCTCGGCGGCTCCCGACAATTAATT	1170 TGGCGGGAACTGTTTTATTCCCGCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAA 1229 	1230 GCTCTATACATCAGTGGAGAATGCTCAGCAGATAAGGGTGTTGCTATCCCCCACGATAT 1289 

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DNA (AAT27110) coding for the 62K antigen (AAR96092) of hepatitis E virus (HEV) Mexico strain capsid protein was cloned into baculovirus expression vector pBluBacIII and recombinant 62K was expressed in 549 insect cells. High levels of expression were obtd. and the recombinant 62K was obtd. in over 95% purity. However, C-terminal processing resulted in the deletion of 9 or 23 amino acids from 62K, giving 2 related polypeptide species (AAR96102 and AAR96101 similar results were obtd. with HEV Burma 62K antigen (see also AAR96101 and AAR96103). Recombinant 62K represents an improved antigen, in comparison to bacterial expressed proteins, for use in HEV diagnostic assays, and also has excellent immunogenic properties. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus (HEV) antigens derived from ORF 2 - useful as diagnostic reagents for determining HEV infection and in vaccines.
                                                                                                                                                                                                                                                             Zhang Y;
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                                                                                                                           (GENE-) GENELABS TECHNOLOGIES INC.
95US-00542634.
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qa	320	eAspLeuGlyAspSerArgValVallleGlnAspTyrAspAsnGlnHisGluGlnAspAr 340
ζ	1350	GCCCACCCCTCGCCTCCCCCTTTTCTGTTCTCCGAGCAAATGATGTACT 1409
Dp	340	gProThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLe 360
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qq	360	uTrpLeuSerLeuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPr 380
ò	1470	GGITTATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCACAGGCCGTAGC 1529
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ò	1530	CCGAICGCIIGACIGGICCAAAGICACCCICGACGGGCGCCCCCCCGACIGIIGAGCA 1589
Dþ	400	aArgSerLeuAspTrpSerLysValThrLeuAspGlyArgProLeuProThrValGluGl 420
λ̈	1590	AINTICCAAGACATICTITGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGAAGGCCGG 1649
qq	420	nTyrSerLysThrPhePheValLeuProLeuArgGlyLysLeuSerPheTrpGluAlaGl 440
δ	1650	CACAACAAAAGCAGGTTATCCTTATAATTATAATACTACTGCTAGTGACCAGATTCTGAT 1709
qq	440	yThrThrLysAlaGlyTyrProTyrAsnTyrAsnThrThrAlaSerAspGln1leLeu11 460
δλ	1710	TGAAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACCACCAGGCTTGGGGCCGG 1769
Db	460	eGluasnalaalaGlyHisargValalaIleSerThrThrThrThrArgLeuGlyAlaGl 480
δ	1770	TCCGGTCGCCATTTCTGCGGCCGCGGTTTTGGCTCCACGCTCCGCCCTGGCTCTGCTGGA 1829
Ob	480	ProvalAlaileSerAlaAlaAlaValLeuAlaProArgSerAlaLeuAlaLeuL
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            ThrSerValGluAsnAlaGlnGlnAspLysGlyValAlaIleProHisAspIleAspLeu
                                                          121 ProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrpLeu
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                                               GGTGATTCGCGTGTGGTCATTCAGGATTATGACAACCAGCATGAGCAGGATCGGCCCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                            SG3 antigen (AAR96094) comprises the C-terminal 327 amino acids of hepatitis E virus (HEV) Mexico strain capsid protein (see also AAR96090). It is obtd. inserting encoding DNA (AAT27112) into pBluescript and ligating the cloned insert into vector pGEX for prodn. of SG3 in E. colicells. SG3 shows low antigenicity compared with capsid 62K antigen (see also AAR96019-22 and AAR96101-04) from HEV Burma and Mexico strains that are produced using a baculovirus expression system. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                  enterically-transmitted non-A/non-B hepatitis virus; vaccine; tosis; antigen.
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in vaccines.
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                                                                                                                                                                                                                                                                                                                                                                      E virus (HEV) antigens derived from ORF 2 - : reagents for determining HEV infection and
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                                                                                             Hepatitis E virus (Mexico strain) SG3 antigen.
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Matches:
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                                                                                                                                                      Hepatitis E virus; Mexico strain
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95US-00542634.
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           AAR96094 standard; protein;
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(first entry)
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N-PSDB; AAT27112.
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Best Local Similarity:
                                                                                                                                                                            WO9612807-A2
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13-OCT-1995;
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06-AUG-1996
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31-DEC-2001; 2001US-00029840.
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                                                                                                                                                                                                                                             A method has been developed for detecting hepatitis E virus (HEV) antibodies (Ab). The method comprises: (a) reacting a serum sample with HBV peptide antigen; and (b) examining the peptide for the presence of bound Ab, where the presence of bound Ab indicates the presence of HEV Ab. The present sequence represents a specifically claimed HBV peptide antigen. The method can be used to diagnose infection with the enterically transmitted non-A/non-B viral hepatitis agent HBV, specifically the HBV Burma and Mexico strains. (Updated on 25-MAR-2003 t correct PF field.) (Updated on 17-OCT-2003 to standardise OS field)
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                 88US-00208997.
89US-00336672.
89US-00367486.
89US-00420921.
9UUS-00505888.
91US-0081078.
92US-0081078.
94US-00240049
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N-PSDB; AAT96966.
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                          11-APR-1989;
16-JUN-1989;
13-OCT-1989;
05-APR-1990;
05-APR-1991;
17-JAN-1992;
 09-MAY-1994;
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TCCCTCACTGCAGCCGAGTATGACCAGTCCACTTACGGGTCGTCAACTGGCCCGGTTTAT 1476
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAGACATTCTTTGTGCTCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACAACA
                                                                                                                                          ATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCGCAGGCCGTAGCCCGATCG
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Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using immuno-assays and nucleic acid hybridisation.
                                                                                                        This sequence represents a Hepatitis E viral hollow particle protein described as ORF2. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptide and nucleic acid allow more accurate detection of HEV than previously possible
                                              ValGluThrSerGlvValAlaGluGluGluAlaThrSerGlvLeuValMetLeuCyElle
AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer
                                                                                         CATGGCTCTCCAGTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG
                                                                                                                                                                                                                                                                                                                                                                Hollow particle protein; virus; antibody; detection; immunoassay;
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                             GITGAGACATCTGGTGGTTGCTGAGGAGGAAGCCACCTCCGGTCT
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Matches:
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Mismatches:
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/label= ORF2
/note= "partial sequence"
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(KOKU-) KOKURITSU YOBO
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Best Local Similarity:
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                                                      The present invention relates to an isolated avian hepatitis E virus having the nucleic acid sequence shown in ABT05872. Vaccines against the virus are also described, and can be used for protecting an avian or mammalian species from viral infection or hepatitis-splenomegaly syndrome caused by the avian or mammalian HEV. The present sequence is a hepatitis E virus protein described in the exemplification of the invention
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Indels:
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Matches:
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                                                                                                                                                                             infection diagnosis, therapy and vaccine development. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis E virus, HEV, SAR-55 strain, enteric transmission, structural region, antigen, detection, antibody; vaccine, immunisation,
                                                                                                                                                                                                                        GINTYTARGValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGly
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                                                                                                                                          US-09-851-410A-10_COPY_5117_7096 (1-1980) x AAR70323 (1-660)
                                                                         Matches:
Conservative:
Mismatches:
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                                                                                                              Indels:
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                                                                                    Percent Similarity:
Best Local Similarity:
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                                Sequence 660 AA
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           LeuProLeuGlnAspGlyThrAsnThrHis1leMetAlaThrGluAlaSerAsnTyrAla
                                                                                                                                             GInTyrArgValAlaArgAlaThrIleArgTyrArgProLeuValProAsnAlaValGly
                                                                                    GGCTATGCTATATCCATTTCTTTCTGGCCTCAAACAACCACAACCCTACATCTGTTGAC
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                                         CAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAATGCAGTTGGA
CTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCCAATTATGCA
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                                                                                                                                                                                                                                           The present sequence is the protein prod, of ORF-2 from the hepatitis E virus (HEV) strain SAR-55, which was implicated in an enterically transmitted non-A, non-B hepatitis in Pakistara. The protein encoded by the structural region of the virus (i.e. ORF-2), which is capable of forming HEV like particles, is useful for the detection of HEV antibodies (pref. 1gG or 1gM) in blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid. The protein, and anti-HEV antibodies generated using the protein, can also be used in vaccines for immunising an animal against HEV infection. The protein is identified as a band of greater than 50 kD following SDS-PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg. Daculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779, -1780 and -1781
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                                                                                                          Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes antigenic protein useful in diagnosis, prophylaxis and treatment of hepatitis E virus infection.
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    RH;
                                                                                                                                                                                                            Claim 6; Page 13-15; 121pp; English
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    Emerson SU,
                                               WPI; 1996-209320/21
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                                                                       N-PSDB; AAT27394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis E virus hollow particle poly:peptide(s) and nucleic acids encoding it - useful for more accurate detection of HEV in samples, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a Hepatitis E viral hollow particle protein. This polypeptide can be used to raise antibodies to detect HEV infection in samples, e.g. by immuno-assay based techniques, and the nucleic acid can be used for the same in nucleic acid hybridisation assays. The polypeptides and nucleic acids allow more accurate detection of HEV than previously possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGTGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGTTCT
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                                            Hollow particle protein; virus; antibody; detection; immunoassay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immuno-assays and nucleic acid hybridisation.
virus hollow particle protein
                                                                                                                                                                                                                                                                                                                                          (DENK-) DENKA SEIKEN KK.
(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Page 24-26; 29pp; Japanese
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                                                                                                                 Hepatitis virus.
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Best Local Similari
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850 CCAGITAACTCCTAIACCAAIACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCC 909
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Search completed: August 16, 2004, 13:48:11 Job time: 114.682 secs λ Q

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Ala 183  GGA 609  GGA 609  GIY 203  GAC 669  Asp 223  GAA 729  GIU 243  GLU 243  TCT 849  TTCT 849  TCT 849  1999  , D.W.; Tam, A.W.  titis E virus (HH	Oy 102 GACCTGCCACACCGGGCTGCGCGC 328  Db 115 AspleutroclintroclyLetArgArg 123  RESULT 4  Structural protein 1 - hepatitis E virus (strain Burma)  C.Species: hepatitis E virus  C.Species: hepatitis E virus  C.Species: bapatitis E virus  A.Stacession: B40778; A40236  R.Yam, A.W. Smith, M.M.; Ouerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.F.  A.Stacession: B40778; A40236  A.Molecule type: genomic RNA  A.Residues: 1-123 cARM>  A.Reference number: A40236  A.Yacossion: B40778  A.Reference number: A40236  A.Yacossion: A40236  A.Yacossion: A40236  A.Yacossion: A40236  A.Reference number: A40236  A.Residues: 1-57, Pr. 59-102, Pr. 104-123  A.Residues: 1-57, Pr. 59-102, Pr. 104-123  A.Residues: 1-57, Pr. 59-102, Pr. 104-123  A.Residues: 1-57, Pr. 59-102, Pr. 104-123  A.Residues: 1-57, Pr. 59-102, Pr. 104-123  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57, Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102, Pr. 104-103  A.Residues: 1-57 Pr. 59-102  C.Superfamily: hepatitis E virus structural protein 1  A.Residues: 1-57 Pr. 59-102  C.Superfamily: hepatitis E virus structural protein 1  A.Residues: 1-57 Pr. 59-102  C.Superfamily: hepatitis E virus structural protein 1  A.Residues: 1-57 Pr. 59-102  A.Residues: 1-57 Pr. 59-102  A.Residues: 1-57 Pr. 59-102  A.Residues: 1-57 Pr. 50-102  A.Residues: 1-57 Pr. 50-102  A.Residues: 1-50-103
NR:AAA45731.1, PID:g330019  trive: 0  ces: 0  123  TGTTTCGCCTATGTCCCGGGCAC 61  TGTTTTCGCCTATGTTGCCGGGCAC 61	15 CysAlaLeuGlyLeuPheCysCysGerSerSerCysPheCysLeuCysCysCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocGerCocG

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R.Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, P.; Bell, J.E.; Sharp, D. A. Biol. Chem. 271, 23547-23557, 1996
A.Title: Protamines of reptiles, A.Reference number: A58208; MUID:96394458; PMID:8798564
        A,Cross-references: GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14880.1; PID:g2635385
A;Experimental source: strain 168
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Cypecies: Herpetosiphon aurantiacus
Cypecies: Herpetosiphon aurantiacus
Cypacesion: 13-7an-1995 #sequence_revision 13-7an-1995 #text_change 13-Jan-1995
Cypacesion: 13-7an-1995 #sequence_revision 13-7an-1995 #text_change 13-Jan-1995
Cypacesion: 13-708
Ryferdann, D.; Duesterhoeft, A.; Kroeger, M.
Bur. J. Biochem. 202, 1247-1256, 1991
A;Title: Cloning and molecular characterization of the HgiCI restriction/ modification shiftle: Cloning and molecular characterization of the HgiCI restriction/ modification shiftles: 19708
A;Reference number: S19706; MUID:92111503; PMID:1662609
A;Status: preliminary
A;Status: DNA
A;Residues: 1-74 <KRO>
A;Cross-references: EMBL:X55138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protamine II - black rat snake (fragment)
C;Species: Blaphe obsoleta quadrivittata
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 07-May-1999
C;Accession: H58208
                                                                                                                                                                A;Pathway: fatty acid biosynthesis
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C;Keywords: fatty acid biosynthesis; ligase
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A,Molecule type: protein
A,Residues: 1-41 <HUN>
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Best Local Similarity:
Query Match:
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C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Accession: T36459
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R;Seession: T36459
A;Rocession: T36459
A;Accession: T36459
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-266 cSEE>
A;Cross-references: EMBL;AL096837; PIDN:CAB48923.1; GSPDB:GN00070; SCOEDB:SCF43A.36
A;Genetics: SCOEDB:SCF43A.36
A;Genetics: A;Genetics: Strain A3(2)
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C; Keywords: structural protein
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Best Local Similarity:
Query Match:
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A;Residues: 1-142 <WHI>
A;Cross-references: GB:AE001921; GB:AE000513; NID:g6458330; PIDN:AAF10219.1; PID:g6458341
A;Experimental source: strain R1
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                                                                                                     hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: D75495
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A;Reference number: A75250; MUID:20036896; PMID:10567266
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C;Superfamily: Deinococcus radiodurans hypothetical protein DR0638
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A;Experimental source: strain WBR-1
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A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                  hypothetical protein 1 (px region) - human T-cell lymphotropic virus type 1 (isolate HAW Cispecies: human T-cell lymphotropic virus type 1, HTLV-1 (Cispecies: human T-cell lymphotropic virus type 1, HTLV-1 (Cispecies: human T-cell lymphotropic virus type 1, HTLV-1 (Cispecies: delegate Reguence_revision 28-oct-1994 #sequence_revision 28-oct-1994 #sequence_revision 28-oct-1994 #sequence_revision 26-oct-1994 #sequence_revision 26-oct-1994 #sequence_revision 26-oct-1994 #sequence_revision 26-oct-1994 #sequence analysis of a provirus derived from HTLV-1-associated myelo A; Reference number: A61547; MUID:88232270; PMID:2897612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: C90345
R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AE006641; NID: 913815078; PIDN: AAK42018.1; GSPDB: GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-99 <TSU>
A,Cross-references: GB:M37301; NID:g541634; PIDN:AAA45390.1; PID:g541637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SSO1819 [imported] - Sulfolobus solfataricus
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A; Residues: 1-104 < KUR>
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A;Gene: SSO1819
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RESULT 15
D87322
hypotherical protein CC0590 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
R;Nierman, W.C.; Feldblyu, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Tile: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Retsis: preliminary
A;Molecule type: DNA
A;Residues: 1-153 <STO>
A;Cossereferences: GB:AE005673; NID:g13421790; PIDN:AAK22576.1; GSPDB:GN00148
C;Genetics:
A;Genetics:
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C;Accession: A46181; B46181
E;Kozalnik, I.J.; Gessain, A.; Klotman, M.E.; Lo Monico, A.; Berneman, Z.N.; Franchini, Proc. Natl. Acad. Sci. U.S.A. 89, 8813-8817, 1992
A;Title: Protein isoforms encoded by the pX region of human T-cell leukemia/lymphotropic A;Reference number: A46181; MUID:92409607; PMID:1528897
A;Accession: A46181
A;Accession: A46181
A;Accusion: Accession: B46181
A;Accession: B46181
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Search completed: August 16, 2004, 13:57:47 Job time : 39.2263 secs

porphyra pu synechocyst synechococc mus musculu zymomonas m oryctolagus candida alb pseudomonas strongyloce arabidopsis caulobacter homo sapien ustilago ma oryctolagus homo sapien cyanidiosch saccharomyc homo sapien exophiala d escherichia chlamydomon mycobacteri

P51371 P74638

054766 Q9wu40

Q9mn5 Q9gm70 Q9czc8 P78589 P28269 Q04073 P10896

norv

rattus

P37136 Q85fy6

P22303

Q15542 P30601 P76398 Q10900

P33413

Q13064 Q92459 Q29499

homo sapien apis dorsat

Q9fec4 Q03164 P01502

Word size:

Sequence: Title: Perfect

Run on:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93079857; PubMed=1448913;
Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,
Bradley D.W., Tam A.W., Reyes G.R.;
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E virus (HEV).";
Virology 191:550-558(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
- THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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CF75E75EFD8FBE2C CRC64;
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01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor.
Hepatitis B vinus (strain Mexico) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
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T2D4 HUMAN
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FDFT_CANAL
OAPT_PSEPU
P3A2_STRPU
RCA_ARATH
EX7L_CAUCR
MKR3_HUMAN
             ACCA_PORPU
ACCA_SYNY3
ACCA_SYNP7
MAN1_MOUSE
DGT1_ZYMMO
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InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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-LDOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=0ligo -TRANS=human40.cdi
-LLST=AE -DOCALLIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODEL-LOCAL
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-NGWINGOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=60 -KGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                          using frame_plus_n2p model
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Ygapop 60.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D

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Result

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### ALTIGNMENT SOURCE:  ### SCORES	241 AlaSerGluLeuValIleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSer  781 GTTGAGACATCTGGTGTGGGGGGGGGCCCTCCGGTCTTGTCATTATGCATA  261 ValGluThrSerGlyValAlaGluGluAlaThrSerGlyLeuValMetLeuCysIle  841 CATGGCTCTCCAGTTAACTCCTATACCAATACCCGTTACTGGCTTACTG  1

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                                                                                                                                                                                                                 MEDINE=92115700; PubMed=1731327;
TSATEV S.A., EMETSON S.U., Reyes G.R., TSATEVA T.S., Legters L.J.,
MAINK I.A., Igbal M., Purcell R.H.;
"Characterization of a prototype strain of hepatitis E virus.";
Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
-!- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
THAR IT MAY BE INVOLUED IN THE ENCAPSIDATION OF THE GENOMIC RNA
                                                                                                                                                                                                                                                                                                                                                                     BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVPA (1-660)
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8085BC53CFB46FD3 CRC64;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Structural protein 2 precursor (ORF2).
Heperlits E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
Hepatitis B-like viruses.
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InterPro; IPR008975; Viral_cap_coat.
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Signal.
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660 AA;
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                                                                                                                                                    NCBI_TaxID=33774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92261377; PubMed=1584074;
Uchida T., Suzuki K., Hayashi N., Iida F., Hara T., Oo S.S.,
Wang C.-K., Shikata T., Ichikawa M., Rikihisa T., Mizuno K.,
Win K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST2_HEVRH (1-485)
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                                                                                                                                                                                                                                                                                          Hepatitis E virus (isolate Rhesus) (HEV).
Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Matches:
Conservative:
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01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1993 (Rel. 27, Last annotation update)
Structural protein 2 (Fragment).
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304 LeuGluLeuGluPheArgAsnLeuThr 312
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InterPro; IPR008975; Viral_cap_coat.
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Best Local Similarity:
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Pred. No.:
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Q00270;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           289 ThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeuAspPheAlaLeuGluLeuGluPhe 308
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                                        GAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCCAGTTAACTCCTAT
                                                                                                                                                                         ACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTGAGTTT
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MEDLINE=92024067; PubMed=1926770;
Tam A.W., Smith M.M., Guerra M.B., Huang C.-C., Bradley D.W.,
Tam A.W., Smith M.M., Guerra M.B., Huang C.-C., Bradley D.W.,
Tam A.W., Smith M.M., Guerra M.B., Huang C.-C., Bradley D.W.,
"Hepatitis E virus (HEV): molecular cloning and sequencing of the
full-length viral genome.";
Virology 185:120-131(1991).
'Virology 185:120-131(1991).
THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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STRUCTURAL PROTEIN 2.
5832A013CCC4A61C CRC64;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-REB-1994 (Rel. 28, Last amoutation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Burma) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
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Mismatches:
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PIR; C40778; VIKWH2.
InterPro; IPR004261; SP2.
InterPro; IPR008975; Viral_cap_coat.
Pfam; PP03014; SP2; 1.
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70978 MW;
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P29326;
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684
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MEDLINE=93227573; PubMed=8470371;
Aye T.T., Uchida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
"Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus Genes 7:95-109(1993).
-!- FUNCTION: CONTENIS A HIGH BASIC AMINO ACID CONTENT SUGGESTING
-!- THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA
BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.
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01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Structural protein 2 precursor (ORF2).
Hepatitis E virus (strain Myannar) (HEV).
Viruses; serna positive-strand viruses, no DNA stage;
NCBI_TAXID=31769;
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STRUCTURAL PROTEIN
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InterPro; IPR008975; Viral_cap_coat.
Pfam; PF03014; SP2; 1.
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660 ST
70998 MW;
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                                                                                                                                                                  177 ArgasnLeuThr 180
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660 AA;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                 004611;
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                                                                                    GGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGGCTGCCTCCCGTCGCC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 CysAlaLeuGlyLeuPheCysCysCysSerSerCysPheCysLeuCysCysProArgHis 34
CCTTTGCCCCAGACGTTGCCGCTGCGGGTCTGGACCTCGCCTTCGCCAACCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IGCGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTGTTTCTGCCTATGTTGCCCGCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsarev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J., Malik I.A., Igbal M., Purcell R.H.; "Characterization of a prototype strain of hepatitis E virus."; Proc. Natl. Acad. Sci. U.S.A. 89:559-563(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Hepatitis E virus (HEV): molecular cloning and sequencing of full-length viral genome."; Virology 185:120-131(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Burma; MEDLINE=92024067; PubMed=1926770; Tam A.W., Smith M.M., Guerra M.E., Huang C.-C., Bradley D.W., Fry K.E., Reyes G.R.; molecular cloning and sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVBU (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M80581; AAA45726.1; -.
PIR; B40778; VHWWHE.
INTECTPO; IPRO03384; HEV_ORF2.
Pfan; PF02444; HEV_ORF2; 1.
SEQUENCE 123 AA; 12676 WW; 8A5A798B1B74EDE5 CRC64;
                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-EBE-1994 (Rel. 28, Last annotation update)
Structural protein I (ORF3).
Hepatitis E virus (strain Burma) (HEV), and
Hepatitis E virus (strain Pakistan) (HEV).
Viruses; SSRNA positive-strand viruses, no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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                                                                                                                                      GACCTGCCACAGCCGGGCTGCGGCGC 328
                                                                                                                                                        or send an email to license@isb-sib.ch).
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NCBI_TaxID=31767, 33774;
                                                                                                                                                                                                                                          STANDARD;
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                                                                    729
                                                                                                                                        789
                                                                                                                                                                    244 LeuVallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThr 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CysAlaLeuGlyLeuPheCysCysCysSerSerCysPheCysLeuCysCysProArgHis 34
                                                                                     GlyTyrAlaIleSerIleSerPheTrpProGlnThrThrThrThrProThrSerValAsp
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 GGCTATGCTATACCATTTCTTGTTGGCCTCAAACAACCACAACCCCTACATCTGTTGAC
                                                                     ATGAATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAA
                                                                                                                                        TTGGTCATCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACA
                                                                                                                                                                                                          TCTGGTGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.B.,
Bradley D.W., Tam A.W., Reyes G.R.,
"Molecular cloning and sequencing of the Mexico isolate of hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVME (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; C44212; C44212.
InterPro; IPR003384; HEV ORF2.
Pfam: PF02444; HEV ORF2; PSEQUENCE 123 AA; 12714 WW, C888F5D638852A68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
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Matches:
Conservative:
Mismatches:
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01-0CT-1993 (Rel. 27, Last sequence update)
01-UTN-1994 (Rel. 29, Last amnotation update)
Structural protein 1.
                                                                                                                                                                                                                                                                                                              123 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    (HEV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=93079857; PubMed=1448913;
                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis E virus (strain Mexico)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M74506; AAA45731.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=31768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus (HEV).
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10-OCT-2003 (Rel. 42, Last annotation update)
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
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    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                   55 SerGlyValThrGlyLeulleLeuSerProSerGlnSerProIlePheIleGlnProThr 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93227573; PubMed=8470371;
Aye T.T., Orbida T., Ma M.Z., Iida F., Shikata T., Ichikawa M.,
Rikihisa T., Winn K.;
"Sequence and gene structure of the hepatitis E virus isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-851-410A-10_COPY_5117_7096 (1-1980) x VST1_HEVMY (1-123)
                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Structural protein 1 (ORF3).
Hepatitis E virus (strain Myanmar) (HEV).
Viruses; ssRAM positive-strand viruses, no DNA stage;
Hepatitis E-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D10330; BAA01173.1; -.
InterPro; IPR003384; HEV_ORF2.
Pfam; PF02444; HEV_ORF2; 1.
SEQUENCE 123 AA; 12751 MW; FB81143F0B31F8A4 CRC64;
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(Rel. 36, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virus Genes 7:95-109(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                            182 CCT 184
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15-JUL-1998
                                                                                                                                                                                                                                                             VST1_HEVMY
Q04612;
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034847;
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C., Brans A., Braun M., Briganell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischi C.V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouillet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Fujita Y., Fume S., Galizzi A., Galleron N.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Mixuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,
RA Takeuchi M., Tamakoshi A., Taragi T., Takahashi H., Takemari K.,
RA Winters P., Wanbutt R., Wedler E., Wedler F., Wealer F., Wanbuet F., Vasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto K., Yasumoto E., Rochiewa H.F., Zamman E., Yoshikawa H.F., Zamman E., Sohikawa H.F., Zammerein B., Yoshikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B., Sohikawa H.F., Zammerein B.
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-:- CATALYTIC ACTIVITY: Carboxybiotin carboxyl carrier protein + acetyl-CoA = biotin carboxyl carrier protein + abonyl-CoA.

-:- PATHMAX: Long-chain fatty acid biosynthesis; first step.
-:- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHEXAMER OF BIOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX (BY SIMILARITY). SIMILARITY: TO THE C-TERMINUS OF MAMMALIAN PROPIONYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lapidus A., Galleron N., Sorokin A., Ehrlich S.D., "Sequencing and functional annotation of the Bacillus subtilis genes
                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98048467; PubMed=9387221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the 200 kb rrnB-dnaB region.".
Microbiology 143:3431-3441(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                   Bacillus subtilis
ACCA OR BSU29200.
                                                                                                                                                                                       NCBI_TaxID=1423;
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Indels:

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SEQUENCE FROM N.A.
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 Query Match:
                                                                                                                                                        RESULT
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-!- FUNCTION: Seems to be the binding site for several of the factors involved in protein synthesis and appears to be essential for accurate translation (89 similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium perfringens.
Bacteria, Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                             US-09-851-410A-10_COPY_5117_7096 (1-1980) x ACCA_BACSU (1-325)
              Subtilist; BG12557; accA.
InterPro; IPR001095; Ac-CoA_carboxylA.
Pfan; PF03255; ACCA; 1.
PRINTS; PR01069; ACCCTRFRASEA.
TIGREMAS; TIGR00513; accA; 1.
Fatry acid biosythesis; Ligase; Complete proteome.
SEQUENCE 325 AA; 36333 MW; 9B177DEE4A5B5864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAF9F83D2C94AC3E CRC64;
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                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-S003 (Rel. 41, Last annotation update)
RPLL OR CPE2414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AA.
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                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                                                                                                                                             294 GGAGGCAGCGGAGGGGCCTGGGCCTG 268
                                                                                                                                                                                                                                                                                                                                                   199 GlyGlySerGlyGlyAlaLeuGlyLeu 207
                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAMAP, MF 00368, -, 1.

InterPro, IPR008932; Ribos_L12/7_olig.
InterPro, IPR00206; Ribosomal_L12.
PFam, PF00542; Ribosomal_L12; I.
ProDom; PD001326; Ribosomal_L12; I.
IIGREAMS; TIGR00855; L12; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=21664373; PubMed=11792842;
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121 AA; 12535 MW;
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100.00%
1.40%
                                                                                                                                                                       4.42
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PIR; G69580; G69580.
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                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flesh-eater.";
                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                CLOPE
                                                                                                                                                                                          Score:
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Conservative: Mismatches:

Matches:

8.00 100.00% 100.00%

Percent Similarity: Best Local Similarity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tollefson A.E., Krajcsi P., Pursley M.H., Gooding L.R., Wold W.S.M., "A 14,500 MW protein is coded by region E3 of group C human adenoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92188523; PubMed=1532104;
Krafosi P., Wold W.S.M.;
"The adenovirus E3-14.5K protein which is required for prevention of
TNF cytolysis and for down-regulation of the EGF receptor contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Down-regulates the EGF receptor and prevents cytolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92263760; PubMed=1533979;

Krajcsi P., Tollefson A.E., Wold W.S.M.;

"The E3-14.5K integral membrane protein of adenovirus that is required for down-regulation of the EGF receptor and for prevention of TNR cytolysis is 0-glycosylated but not N-glycosylated."; Virology 188:570-579(1992).
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                                                                                                                                                                                                                                                                                                              Human adenovirus type 5.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=9218953; PubMed=1531370; Krajcsi P., Tollefson A.E., Anderson C.W., Wold W.S.M.; Krajcsi P., Tollefson A.E., Anderson C.W., Wold W.S.M.; The adenovirus E3 14.5-kilodalton protein, which is required for down-regulation of the epidermal growth factor receptor and prevention of tumor necrosis factor cytolysis, is an integral membrane protein oriented with its C terminus in the cytoplasm."; J. Virol. 66:1665-1673(1992).
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-85092388; PubMed=2981456;
Cladaras C., Wold W.S.M.;
"DNA sequence of the early E3 transcription unit of adenovirus
Virology 140:28-43(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES.
                                      US-09-851-410A-10_COPY_5117_7096 (1-1980) x RL7_CLOPE (1-121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PTM: Phosphorylated on serine; O-glycosylated,
                                                                                                                                                                                                                               01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Early E3B 14,6 kDa protein precursor.
                                                                                                                                                                                             132 AA.
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with the genome of adenovirus type 2."; virology 186:280-285(1992).
                                                                             83 GCCGTCGTGGCGCGCGCGCGCG 106
                                                                                                                                                                                             PRT;
                                                                                                         38 AlaValValGlyGlyAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLETE GENOME.
MEDLINE=92087470; PubMed=1727603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=2309441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL SEQUENCE CLEAVAGE SITE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION OF PROTEIN. MEDLINE=90177214; Pubmed=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 175:19-29(1990).
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93
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eur. J. Blochem. 201:53-59(1991).
-!- FUNCTION: Increases water and sodium absorption in the intestine and gall-bladder.
-!- FUNCTION: Contains 1 SoHo domain.
-!- SIMILARITY: Contains 1 SoHo domain.
--- FIR: S17837, S17837.
--- FIR: PR0031217, Sorb.
--- FIR: Pro2008; Sorb; 1.
--- FroDom; PD016158; Sorb; 1.
                                                                                       InterPro; IPR008131; Adeno_E3_14_5.
Pfam; PF04834; Adeno E3 14_5; 1.
Early protein; Transmembrane; Glycoprotein; Phosphorylation; Signal.
SIGNAL 1 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Intestine;
MEDLINE=92007891; PubMed=1915377;
MEDLINE=92007891; PubMed=1915377;
Vagne-Desoroix M., Pansu D., Joernvall H., Carlquist M., Guignard Jourdan G., Desvigne A., Collinet M., Caillet C., Mutt V.;
"Isolation and characterisation of porcine sorbin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                    US-09-851-410A-10_COPY_5117_7096 (1-1980) x E315_ADE05 (1-132)
                                                                                                                                   EARLY E3B 14.6 kDa PROTEIN
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                                                                                                                                                POTENTIAL.
524690C4AD9B9A74 CRC64;
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Indels:
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Conservative:
Mismatches:
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             153 AA
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Matches:
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EMBL; X03002; CAA26786.1; -.
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14750 MW;
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AA; 17481 MW;
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                                                                                                                                             51
132 AA;
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Best Local Similarity:
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Pred. No.:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Sorbin.
                                                                                                                                                                                                                                  Query Match:
DB:
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SORB PIG
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119 CCACCGCCGGTACCGCCGCTGCGC 96

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Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McGeoch D.J., Cunningham C., McIntyre G., Dolan A.;
"Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2.";
J. Gen. Virol. 72:3057-3075 (1991).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL3,
HSV-2 UL3, BHV-1 60, AND VZV 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-851-410A-10_COPY_5117_7096 (1-1980) x UL03_HSV2H (1-233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005035; Herpes UL3.
Pfam; PF03369; Herpes UL3; 1.
SEQUENCE 233 AA; 25649 MW; B38F613BD839AA24 CRC64;
                                                                                                                                                                                                                                                                             Herpes simplex virus (type 2 / strain HG52).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
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Matches:
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S2.
                                                                                                                    Last sequence update)
Last annotation update)
    233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92113549; PubMed=1662697;
                                                                                                                                                                                                                                                                                                                                                            Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=10315;
                                                                              Created)
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STANDARD;
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01-DEC-1992
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    UL03 HSV2H
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P51249;
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                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-i. FUNCTION: Major function may be to aid in digestion of the blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Midgut.
-!- SIMILARITY: Belongs to peptidase family S1.
             Plant Mol. Biol. Rep. 13:333-335(1995).
-!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
NCBI TaxID=7159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97242546; PubMed=9087545;
Kalhok S., Tabak L.M., Prosser D.E., Brook W., Downer A.E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-851-410A-10_COPY_5117_7096 (1-1980) x RR2_PORPU (1-241)
                                                                                                                                                                                                                                                                                                                                                                                 FA17DA9C352FC866 CRC64;
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Matches:
Conservative:
Mismatches:
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01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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INTERPRO; IPR001865; Ribosomal S2.

INTERPRO; IPR001865; Ribosomal S2.

INTERPRO; IPR00180; Ribosomal S2.

PEAM; PP00318; Ribosomal S2; 1.

PRINTS; PR00395; RIBOSOMĀLS2.

TIGRFAMS; TIGR01011; rpsB bact; 1.

PROSITE; PS00962; RIBOSOMĀLS2.

RIBOSOMAL S2 2; 1.

RIBOSOMAL S2 2; 1.

RIBOSOMAL S2 2; 1.
                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypsin 3A1 precursor (EC 3.4.21.4). Aedes aegypti (Yellowfever mosguito)
                                                                                                                                                                                              EMBL; U38804; AAC08135.1; -.
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Percent Similarity:
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TRY3_AEDAE
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BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
43AAF13BBDE7D485 CRC64;
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                 Promission involution reputable SIA.

Prints, PR00099; trypsin; 1.

PRINTS, PR00072; CHYMOTRYSIN.

SMART; SM00072; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; PALSE NEG.

PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Serine protease; Signal; Zymogen; Digestion; Multigene family.
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ACTIVATION PEPTIDE.
TRYPSIN 3A1.
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Job time : 26.2362 secs
                           MEROPS, F00763, IDPO.
MEROPS, S01.112, -.
InterPro; IPR009003, Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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EMBL; X64362; CAA45714.1;
PIR; S19890; TRWV3Y.
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Best Local Similarity:
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Patent No. 5686239
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Tam, Albert W.
APPLICANT: Tarbough, Partice O.
TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods NUMBER OS EQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
COMPUTER: TEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,049B
FILING DATE: 09-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Charles K. Sholtz
REGISTRATION NUMBER: 39 6155
REGISTRATION NUMBER: 39 6155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4
TELECOMMUNICATION INFORMATION:
         US-07-870-985A-18

US-08-542-634-16

US-08-542-634-26

US-08-542-634-26

US-08-542-634-28

US-08-542-634-28

US-08-240-049B-14

US-08-240-049B-14

US-08-259-148A-16

US-08-484-054-16

US-08-484-054-16

US-08-484-054-18

US-08-487-292-18

US-08-477-292-18

US-09-172-699-20

US-09-172-699-20

US-09-462-606-51

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TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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-Q=/cgn2 1/USPF0 spool p/USO881410/runat 16082004 125718 9682/app query.fasta_1.4238
-DB-Issued Patents AA -OPMT=fastan -SUFFX=01i.rai -MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=01igo -TRANS=human40.cdi
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-USFR=10509851410 @CGN 1_1 -45 @runat -16082004 125718 9682 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBADCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOX=7
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               - protein search, using frame_plus_n2p model
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US-07-876-941A-20
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US-08-542-634-14
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US-08-542-66-48
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281 HisGlySerProValAsnSerTyrThrAsnThrProTyrThrGlyAlaLeuGlyLeuLeu
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  ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle
                                                                            GACTITGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACACAATACACGTGTG
                                                                                           TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HE
INDIVIDUAL ISOLATE: OR
                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                        US-08-240-049B-16
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Matches:
Conservative:
Mismatches:
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                     Percent Similarity:
Best Local Similarity:
Query Match:
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                                                     SerThrValhlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 659
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APPLICANT: Reves, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jr. Shin
APPLICANT: Twn, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Yaraczynski, Krzysztof Z.
APPLICANT: Yarbough, Patrice D.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: JSO Cambridge Rassociates
STREET: JSO Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              629
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPANE: IBM PC compatible
COMPANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
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FILING DATE: 13-0CT-1989
FILING DATE: 13-0CT-1989
FRIDK APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UW-1989
FRIDK APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APR-1989
FRIDK APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UW-1988
ATTORNEY/AGENT INFORMATION:
NAWE: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 38,615
REGISTRATION INFORMATION:
TELEPOMOWICATION INFORMATION:
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TELEPOMOWICATION INFORMATION:
TELEPOMOWICATION INFORMATION:
TELEPOMOWICATION INFORMATION:
                                                                                                                                                                               Sequence 20, Application US/08259148A Patent No. 5741490 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
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Pred. No.:
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COUNTRY:
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                                                                                                                                                                                    GlyLeuProThrGluLeuIleSerSerAlaGlyGlyGlnLeuPheTyrSerArgProVal
                                                                                                                                                                                                                                                                                                            421 AsplysGlyValAlaIleProHisAspIleAspLeuGlyAspSerArgValValIleGln
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US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-484-054-20 (1-659)
                APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Michael A.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
APPLICANT: Krawczynski, Krzysztof Z.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                           3: Dehlinger & Associates
350 Cambridge Avenue, Suite
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 367, 486
FILING DATE: 16-UUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 17-UUNE-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 870,985
FILING DATE: 20-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
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TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    659.00
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CITY: Palo Alto
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Best Local Similarity:
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ATGCGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTGTTTCTGCCTATGTTGCCCGCGCCCA 60

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Sequence 20, Application US/08484054 Patent No. 5770689 GENERAL INFORMATION: APPLICANT: Reyes, Gregory R.

	361 GlyGluValGlyArgGlyIleAlaLeuThrLeuLeuAsmLeuAlaAspThrLeuLeuGly 380  1141 GGGCTCCCGACAGAATTAATTCGTCGCCGGCGCACTGTTTTATTCCCGCCCG	461 PheSerValleuArgAlaAsnAspValleuTrpleuSerleuThrAlaAlaGluTyTASp 480  1441 CAGTCCACTTACGGGTCGTCAACTGGCCGGTTTATATCTCGGACAGCGTGACTTTGGTG 1500  481 GlnSerThrTyrGlySerSerThrGlyProValTyr1leSerAspSerValThrLeuVal 500  1501 AATGTTGCGACTGGCGCAGGCCGTAGCCCGATGGTTGGTCAAAGTCACCTC 1560  501 AATGTTGCGACTGGCGCAGGCCGTAGCCCGATGGTTGACTCGTCAAAGTCACCTC 1560  1561 GACGGCGCCCCCCCCCGACTGTAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTT 1620  1561 GACGGCGCCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTT 1620  1571 GACGGCGCCCCCCCCCCCAACTGTGAGCAATATTCCAAGACATTTTTTGGCAGCTTTTTTTT	ArgGlyLysLeuSerbheTrpGluAlaGlyThrIhysAlaGlyThrIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	1921 TCAACTGCTGAGCTCTAAAGTTAAGGTGGGTAAACTCGGGAGTTG 1977  1921 TCAACTGCTGGCTCAGCGCCTTAAAGTTAAGGTGGGTAAACTCGGGGAGTTG 1977  641 SerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu 659  44  456-941A-20  bit No. 5885768  FRAL INFORMATION:  PPLICANT: Reyes, Gregory R.  PPLICANT: Tam, Albert W.  PPLICANT: Tam, Albert W.  PPLICANT: Mitchell, Carl  TLE OF INVENTION: Antibodies  MNBER OF SEQUENCES: 76  RRESPONDENCES: 76  ADDRESSEE: Dehlinger & Associates  STREET: 350 Cambridge Avenue, Suite 250
	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 8 8 8 8 8 8 8	3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	Cy Cy Db RESULT US-GOT-E I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I Sequent I
	MetArgProArgProLeuLeuLeuLeuPheLeuPheLeuProMetLeuProAlaPro CCGACCGGTCAGCCGTCGTCGGGGGGGGGGGGGGGGGGG		AATTATGCACAGTACCGGGGTTGCCCGGGCTTACCGGTGCGGGCCCTAGTGCCGAATTATGCACAGTACCGGGCCGGGGTTGCGGGGCCTAGTGCGGGCCCTAGTGCGGGCCTAGTGCGGGGGGGG	ValGluThrEstGlyvalAlaGluGluGluAlathrSerGlyLeuValMetLeuCyslle ValGluThrEstGlyvalAlaGluGluGluAlathrSerGlyLeuValMetLeuCyslle CarceCcactcrCcCattacCattacCattacCattacCacttacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacCattacC

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TCCCGTTACTCCAGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTG 1020
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                                              241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCCAGGCGCCCTCCGCTGCCTCCGTCGC
                                                                           AATTATGCACAGTACCGGGGTTGCCCGCGCTACTATCCGGTTACCGGCCCCTAGTGCCTAAT
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                                                                                                                MUDLUM TIKE: FIGHTY ALLER
MUDLUM TIKE: FIGHTY ALLER
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
RIING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 13-COCOBER-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-AUNE-1988
ATIONEWAY-ACKNATION:
ANAMER: NO-ALTER FERENCE FELLING DATE: NAME-1848
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ANAMER: NO-ALTER FELLING DATE: NAME-1848
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Matches:
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Gaps:
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REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INPORMATION:
TELEPAN: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
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   amino acid
GY: linear
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 943.06
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOOPPY di
COMPUTER: IBM PC comp
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                           Hepatitis E Virus (Mexico Strain)
ORF-2
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Conservative:
Mismatches:
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APPLICATION NUMBER: US/08/327,952
                                              NAME: Brookes, Allan A
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: 33295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 369-9500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 659 amino acids
TYPE: amino acid
TYPE: amino acid
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                                   ATTORNEY/AGENT INFORMATION
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Best Local Similarity:
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              FILING DATE:
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Pred. No.:
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                                         441 AspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fuerst, Thomas
APPLICANT: Actee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis E Virus
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08477292
Patent No. 6291641
GENERAL INFORMATION:
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STREET: 505 Penobscot Drive
CITY: Redwood City
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PRIOR APPLICATION DATA:
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                                       581 SerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeu
                                                                                                                                                                          621 ThrPheAspAspAspPheCysProGluCysArgAlaLeuGlyLeuGlnGlyCysAlaPheGln
                                                                                     Sequence 20, Application US/07870985A

| Patent No. 6455492
| GENERAL INPORMATION:
| APPLICANT: Bradley, Daniel W. APPLICANT: Twu, Jr-Shin
| APPLICANT: Purdy, Michael A. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Tam, Albert W. APPLICANT: Krawczynski, Krzysztof Z. APPLICANT: Correspondence: 22 CORRESPONDENCE: 22 CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,985A
FILING DATE: 20-APRIL-1992
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350 Cambridge Avenue, Suite
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APPLICATION NOMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 420,921
PILING DATE: 13-OCYOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-UUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
PILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-JUNE-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Palo Alto
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US-07-870-985A-20
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                                                                                                                                             AATCCGCCTCTGCCGCTGCAGGACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC
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                                                                                                                                    ATGCGCCCTAGGCCTCTTTTGCTGTTGTTCCTCTTGTTCTGCCTATGTTGCCCGCGCCA
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Matches:
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659.00
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  amino acids
LENGTH: 659 amino acidi
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: OR
                                                                                   Percent Similarity:
Best Local Similarity:
                                                 US-07-870-985A-20
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Ω	261	ValGluThrSerGlyValAlaGluGluGluAlaThrSerGlyLeuValMetLeuCysIle 280
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Д	341	ThrThrThrAlaAlaThrArgPheMetLysAspLeuHisPheThrGlyLeuAsnGlyVal 360
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λ.	1321	1 1 1
ρ	441	AspTyrAspAsnGlnHisGluGlnAspArgProThrProSerProAlaProSerArgPro 460
<u>ہ</u> .	1381	TITICIGITCECGAGCAATGATGTACTITGGCTGTCCCTCACTGCCGGCCGAGTATGAC 1440
Ω	461	Pheservalleuargalaashaspvalleuirpleuserleuinralaalasuuiyrasp 460
≱ a	1441	.441
<b>≽</b> ,	1501	AATGTTGCGACTGGCGGCGGCAGGCCGTAGCCCTTGACTGGTCGGTC
۵	501	AsnvalalaThrGlyAlaGlnAlaValAlaArgSerLeuAspTrpSerLysValThrLeu 520
<u>≻</u>	1561	GACGGGGGCCCTCCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCCTT 1620
മ	521	AspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuProLeu 540
<u>~</u>	1621	CGTGGCAAGCTCTCTTTTGGGAGGCCGGCACAACAAAAGCAGGTTATCCTTATAATTAT 1680
۵	541	ArgGlyLysLeuSerPheTrpGluAlaGlyThrThrLysAlaGlyTyrProTyrAsnTyr 560
<u>≯</u> .	1681	
۵	561	AsnīhrīhrālaSerAspGlnīleLeuīleGluAsnālāālaGlyHisArgValālaīle 580
Δ	1741	TCAACCTATACCACCAGGCTTGGGGCCGGTCCGGTCGCCATTTCTGCGGCCGCGGGTTTTG 1800
മ	581	SerThrTyrThrThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeu 600
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                                                                                                                                                                             TrpProGlnThrThrThrThrProThrSerValAspMetAsnSer11eThrSerThrAsp 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                          341 ThrProSerProAlaProSerArgProPheSerValLeuArgAlaAsnAspValLeuTrp 360
      41 AsnLeuValLeuTyrAlaAlaProLeuAsnProProLeuProLeuGlnAspGlyThrAsn 60
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                                                                   ACTCACATTATGGCCACAGAGGCCTCCAATTATGCACAGTACCGGGTTGCCCGCGCGCTACT
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                        641 SerThrValAlaGluLeuGlnArgLeuLysValLysValGlyLysThrArgGluLeu
1921 TCAACTGTCGCTGAGCTCCAGCGCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG
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CORRESPONDENCE ADDRESS:
ADDRESSEE Cathleen M. Desjardins, M.D.
STREET: 505 Penobscot Drive
CITY: Redwood City
STAIE: CA
COUNTRY: US
ZIP: 94663
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEMP PC COMPATIBLE
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PatentIn Release #1.0, Version #1.25
COMPUTER: PATENTIN DATA:
APPLICATION NUMBER: US/08/477,292
FILING DATE:
APPLICATION NUMBER: US/08/327,952
FILING DATE:
ATTORNEY/AGENT INFORMATION:
AMANE: BEFORKER/DOCKET NUMBER: 36,373
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 36,373
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US-08-477-292-16
; Sequence 16, Application US/08477292
; Patent No. 6291641
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                                                                                                                                                                                           APPLICANT: Fuerst, Thomas
APPLICANT: McAtee, Patrick
APPLICANT: Yarbough, Patrice
APPLICANT: Zhang, Yifan
TITLE OF INVENTION: Hepatitis
NUMBER OF SEQUENCES: 24
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity:
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E Virus (Mexico Strain)
  Hepatitis
ORF-2
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99.55%
99.55%
77.69%
; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-542-634-14
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Best Local Similarity:
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                                     TCCAAGACATTCTTTGTGCTCCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGGCACA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fuerst, Thomas R.
APPLICANT: McAtee, C. Patrick
APPLICANT: Yarbough, Patrice O.
APPLICANT: Transport, Stian
TITLE OF INVENTION: HEPATITIS E VIRUS AN
NUMBER OF SEQUENCES: 31
CORRESSPONDENCES ADDRESS:
ADDRESSEE: Dehlinger & Associates
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STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
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CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Fablan, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08542634; Patent No. 6214970; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
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TOPOLOGY:
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                                                                                                                   US-09-851-410A-10_COPY_5117_7096 (1-1980) x US-08-542-634-14 (1-660)
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                                 Conservative:
Mismatches:
Length:
Matches:
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CCGACCGGTCAGCCGTCTGGCCGCCGTCGTGGGCGGCGCAGCGGCGGTACCGGCGGTGGT 120
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1 MetArgProArgProLeuLeuLeuLeuPheLeuLeuPheLeuProMetLeuProAlaPro
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                                                  RESULT 9
PCT-US95-13703-14
; Sequence 14, Application PC/TUS9513703
; GENERAL INFORMATION:
; TITLE OF INVENTION: USES THEREFOR
; TITLE OF INVENTION: USES THEREFOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Deblinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
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COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13703
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Mismatches:
Indels:
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Matches:
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ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION UNBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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amino acid
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
DB:
1977 G 1977
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             GACTITGCCTTAGAGCTTGAGTTTCGCAATCTCACCACCTGTAACACACAATACACGTGTG
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                           rLeuAspGlyArgProLeuProThrValGluGlnTyrSerLysThrPhePheValLeuPr
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241 CGGCCACTTGGCTCCACTTGGCGAGATCAGGCCCAGCGCCCCTCCGCTGCCTCCCGTGC 300	1 CGACCTGCCACAGGGGGGCTGCGGGGCTGTGGGCGCTGCCTGC	CCGTCCCGGACGTTGATTCTCGCGGTGCAATTCTACGCCGCCAGTATAATTTGTCTACT	21 FrovalFroAspvalAspSelAigGiyAlalleLeuAigArgGilliyrAshLeuS 21 TCACCCCTGACATCCTGTGGCCTCTGGCACTAATTTAGTCCTGTATGCAGCCC 41 SerProLeuThrSerSerValAlaSerGlyThrAshLeuValLeuTyrAlaAlaP	481 AATCCGCCTCTGCAGCACGGTACTAATACTCACATTATGGCCACAGAGGCCTCC 540	541 AATTATGCACAGTACCGGGTTGCCCGCGCTACTATCCGTTACCGGCCCCTAGTGCCTAAT 600 	GCAGTTGGAGGCTATGCTATTCTTTCTGGCCTCAACAACCAAC	TCTGTTCACATGATTCCATTACTTCCACTGATGTCGCGATTCTTGTTCAACCTCGCCATA	1 GCATCTGAATTGGTCATCCAAGGAGGCCTTCACACACCAATCAAGGTTGGCGCTCG	81 GTTGAGACATCTGGTGTTGCTGAGGAGGAAGCACCTCCGGTCTTGTCATGTTATGCATA	841 CATGGCTCTCCAGTTAACCTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTG 900	901 GACTITGCCTIAGAGCTIGAGTITCGCAAICTCACCACCTGIAACACCAAIACACGTGIG 960 	961 TCCCGTTACTCCAGCACTGCTCACTCCGCCCGAGGGGCCGACGGGACTGCGGA 1016 	1017 GCTGACCACAACTGCAGCCACCAGGTTCATGAAAGATCTCCACTTTAACGGCCTTAATGG 1076 	1077 GGTAGGTGAAGTCGGCGGGGATAGCTCTAACTTAACCTTGCTGCGCGCCCCT 1136 	1137 CGCCGCCTCCCCACAAATTAATTTCGTCGCTGGCGGCAACTGTTTTATTCCCCCCCC	1197 GGTTGTCTCAGCCCAATGGCGAGCCAACCGTGAAGCTCTATACATCAGTGGAGAATGGTCA 1256 	1257 GCAGGATAAGGGTGTTGCTAICCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCAT 1316 	1317 TCAGGAITAIGACAACCAGCAIGAGCAGGATCGGCCCACCCCGTCGCCTGCGCCAICTCG 1376

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GCTATCCCCCACGATATCGATCTTGGTGATTCGCGTGTGGTCATTCAGGATTATGACAAC 1332
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                                      21 VallleProSerGluArgLeuHisTyrArgAsnGlnGlyTrpArgSerValGluThrSer
                                                                                                      GTTAACTCCTATACCAATACCCCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTA
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                   GICALCCCAAGCGAGCGCCTTCACTACCGCAATCAAGGTTGGCGCTCGGTTGAGACATCT
                                                                                      GGTGTTGCTGAGGAAGCCACCTCCGGTCTTGTCATGTTATGCATACATGGCTCTCCA
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                                                                    Krawczynski, Krzysztof Z.
Yarbough, Patrice D.
WENTION: Hepatitis E Virus Vaccine and Method
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0 0 0
0 0 0
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 05-APR-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 13-OCT-1989
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Mismatches:
Indels:
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FILING DATE: 11-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNN-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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 Bradley, Daniel W.
Twu, Jr-Shin
Purdy, Michael A.
Tam, Albert W.
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APPLICANT: Bradley, Dan:
APPLICANT: Twu, Jr-Shin
APPLICANT: Purdy, Micha
APPLICANT: Tam, Albert I
APPLICANT: Krawczynski,
APPLICANT: Krawczynski,
APPLICANT: Yarbough, Pat
ITLE OF INVENTION: Hepp
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-OCT-7
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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INDIVIDUAL ISOLATE:
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Best Local Similarity:
                                                                                                                                                                                                                          USA
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Pred. No.:
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                                                                                                                                                                                                                          COUNTRY:
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DB:
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380

ThrArgLeuGlyAlaGlyProValAlaIleSerAlaAlaAlaValLeuAlaProArgSer

361

732 20

AATTCCATTACTTCCACTGATGTCAGGATTCTTGTTCAACCTGGCATAGCATCTGAATTG AsnSerlleThrSerThrAspValArg1leLeuValG1nProG1yIleAlaSerG1uLeu

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Alignment Scores:
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                                                   1873 TICTGCCCTGAATGCCGCGCTTTAAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCT
                                                                                 1933 GAGCTCCAGCCCTTAAAGTTAAGGTGGGTAAAACTCGGGAGTTG 1977
                                                                                            Sequence 18 Application US/08484054

Statent No. 5770689

GENERAL INFORMATION:
APPLICANT: Reves, Gregory R.
APPLICANT: Twu, Jr.Shin
APPLICANT: Twu, Jr.Shin
APPLICANT: Twu, Albert M.
APPLICANT: Tam, Albert M.
APPLICANT: Hepatitis B Virus Vaccine and Method
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                          COUNTRI:

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,054
PTI.NG DATE: 07-UUN-1995
                                                                                                                                                                                                                                             STREET: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                US 208,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
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LENGTH: 435 amino acids
TYPE: amino acid
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                                                                                                                        RESULT 12
US-08-484-054-18
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Mismatches:
Indels:
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Matches:
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100.00%
100.00%
66.01%
                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                 ; INDIVIDUAL ISOLATE:
US-08-484-054-18
linear
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Best Local Similarity:
Query Match:
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Alignment Scores:
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                                                     CICCCGACTGTTGAGCAATATTCCAAGACATTCTTTGTGCTCCCCTTCGTGGCAAGCTC 1632
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                                                                                                          TCCTTTTGGGAGGCCGGCACAACAAAGCAGGTTATCCTTATAATTATAATACTACTGCT 1692
                                                                                                                                                             AGTGACCAGATTCTGATTGAAATGCTGCCGGCCATCGGGTCGCCATTTCAACCTATACC 1752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reyes, Gregory R. APPLICANT: Bradley, Daniel W. APPLICANT: Tam, Albert W. APPLICANT: Mitchell, Carl TITLE OF INVENTION: Hepatitis E VI TITLE OF INVENTION: Antibodies NUMBER OF SEQUENCES: 76 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-876-941A-18; Sequence 18, Application US/07876941A; Patent No. 5885768; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILLING DATE: 16-UTURE-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 822,335 FILING DATE: 17-JAN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 505,888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 420,92 FILING DATE: 13-OCTOBER-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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973 AGCACTGCTCGTCACTCCGCCCGAGGGGCCGACGGGACTGCGGAGCTGACCACAACTGCA 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
             FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-UNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION 108: 18:
FERENCE (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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    US 336,672
                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: li-
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100.00%
100.00%
66.01%
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INDIVIDUAL ISOLATE:
APPLICATION NUMBER:
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973 AGCACTGCTCGTCACTCCGCCCGAGGGCCGACGGGACTGCGAGCTGACCACAACTGCA 1032
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Mismatches:
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Matches:
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      CONKENT AFFLICATION UNDERS. 315
PELING DATE: 20-APRIL-1992
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
PRIOR APPLICATION NUMBER: US 367,486
PRIOR APPLICATION NUMBER: US 367,786
PRIOR PAPLICATION NUMBER: US 316,672
PRIOR APPLICATION NUMBER: US 316,672
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REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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US-07-870-985A-18
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Best Local Similarity:
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APPLICANT: Bradley, Daniel W.
APPLICANT: Twu, Jarshin A.
APPLICANT: Twu, Jarshin A.
APPLICANT: Tam, Albert W.
APPLICANT: Tam, Albert W.
TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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; Sequence 18, Application US/07870985A
Patent No. 6455492
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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THEREFOR

E: Dehlinger & Associates 350 Cambridge Ave., Suite 250

Palo Alto

USA

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APPLICANT: Zhang, Yifan
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES
NUMBER OF SECRENCES: 31
CORRESPONDENCE ADDRESS:
                                        ADDRESSEE:
STREET: 35
                                                                      STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            Score:
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0 0
1 3
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ZIP: 94306
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DAYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,634
FLING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0890
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels:
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amino acid
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99.45%
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                           LENGTH:
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Sequence 16, Application US/08542634
Patent No. 6214970
GENERAL INFORMATION:
APPLICANT: Fuerst, Thomas R.
APPLICANT: Makee, C. Patrick
APPLICANT: Yarbough, Patrice O.

RESULT 15 US-08-542-634-16

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777 753 Jel 1 SCC 813     1 I 1 1 60 NCC 873	hr 180 17 933 19 200 17 989 1 220	AC 1109 Th 260 GC 1169	122 300 300 320	CG 1349     1349   Ar 340   CT 1409   Le 360   CC 1469	57 380 57 1529 11 400 1589 51 420	1649 11440 111709 11460 11480 11480
TCAACCTGGCATAGCATCTGAATTGGTCATCCCAAGCGAGCG	TProvalAenSerTyrThrAsnTh CTTAGAGCTTGAGTTTCGCAATCTC ALeuGluLeuGluPheArgAsnLeu CTCCAGCACTGCTCGTCACTC 	CAACTGCAGCCACCAGGTTCATG	AGCCAATGGGGGGGCGACCATGGGGGGGGGGGGGGGGGG		rfhrTyrGlySerSerfhrGly, TGCGACTGGCGCGCAGCCGTAC [	CAAGCTCCTTTTGGGAGGCCGG
F-6 4-5 F-	ThrSerGlyLeuvalMetieuCysileHisGlySerProvalAsnSerTyrthrAsnTh CCTTATACCGGTGCCCTTGGCTTACTGGACTTTGCCTTAGAGCTTTGGCAATCT [	CGCCCGAGGGCCGACGGGACTGCGGAGCTGACCACTGCAGCCACCAGCTCATGAA	TGGCGGGCAACTGTTTTATTCCCGCCCGGTTGTCTCAGCCAATGGCGAGCCAACCGTGAA aG1yG1yG1nLeuPheTyrSerArgProValValSerAlaAsnG1yG1uProThrValLy GCTCTATACATCGGGAGATGCTCAGCAGGATAAGGGTTGCTTGC	CONTINUED TO CONTINUED TO CONTINUED AND CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONTINUED TO CONT	euSerleuThrAlaAlaGluTyrAspGlnSerThrTyrGlySerSerThrGlyPr ATATCTCGGACAGCGTGACTTTGGTGAATGTTGCGACTGGCGCAGCCGTAGC	ATATTCCAAGACATTCTTGTGCTCCCCTTCGTGGCAAGCTCTCCTTTTGGGAGGCCGG [
94 GTCAGGATTCTT 21 ValargileLeu 54 CACTACGGCAAT 41 HisTyrArgAsn 14 ACCTCCGGTCTT	161 ThrSerGlyLeuv 874 CCTTATACCGGTG              181 ProTyrThrGlyA 934 ACCACCTGTAACA 201 ThrThrCysAsnT	990 CGCCCGAGGGCCC 	1170 TGGGGGGAACTG	10 10	360 uTrpLeuSerLeuf 1470 GGTTAPATCTCGG	1590 ATATTCCAAGACAT 420 ITYTSETLYSTHIF 1650 CACAACAAAAGCAG 1440 YTHTHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI

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480 yProvalala1leSerAlaAlaValLeuAlaProArgSerAlaLeuLeuG 500	1830 GGATACTITIGATTATCCGGGCGCGCGCACACATTGATGACTTCTGCCCTGAATGCCG 1889	500 uAspIhrPheAspIyrProGlyArgAlaHisThrPheAspAspPheCysProGluCysAr 520	1890 CGCTTTAGGCCTCCAGGGTTGTGCTTTCCAGTCAACTGTCGCTGCAGCTCCAGCGCCTTAA 1949		1950 AGTTAAGGTGGGTAAAACTCGGGAGTTG 1977	540 sVallysValGlyLysThrArgGluLeu 549	
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